

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:23:01 ; Search time 16.31 Seconds  
(without alignments)  
871.933 Million cell updates/sec

Title: US-09-016-869b-35

Perfect score: 760

Sequence: 1 MEPSADMWMTAAARGVREEV.....TRGSNHRIDAAEGPSDIPD 148

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

T number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	753	99.1	156	2 JE0141	cyclin dependent k
2	529	69.6	130	2 I78845	p15INK4b - mouse
3	522	68.7	138	2 B55479	CDK4 inhibitor p14
4	461.5	60.7	167	2 I58352	p16INK4a - mouse
5	258	33.9	164	2 A57378	cyclin-dependent k
6	249	32.8	166	2 A57379	CDK4/CDK6 inhibito
7	244	32.1	166	2 B57378	cyclin-dependent k
8	231.5	30.5	168	2 B57379	CDK4/CDK6 inhibito
9	228.5	30.1	168	2 A55479	CDK6 inhibitor p18
10	209	27.5	41	2 I52720	gene p15INK4b prot
11	158	20.8	3924	2 S37431	ankyrin 2, neutroa
12	137.5	18.1	1848	2 S37771	ankyrin, erythrocy
13	137.5	18.1	1862	2 I49502	ankyrin - mouse
14	133.5	17.6	1856	2 B35049	ankyrin 1, erythro
15	133.5	17.6	1880	2 A35049	ankyrin 1, erythro
16	133.5	17.6	1881	1 S3HUK	ankyrin 1, erythro
17	131	17.2	857	2 S62694	potassium channel
18	130.5	17.2	1423	2 I37275	death-associated p
19	130	17.1	838	2 S33606	potassium channel
20	130	17.1	1765	2 T42715	ankyrin 3, splice
21	130	17.1	1940	2 T42715	ankyrin 3, splice
22	130	17.1	1943	2 T42715	ankyrin 3, splice
23	130	17.1	1961	2 T42716	ankyrin 3, splice
24	128	16.8	4377	2 A55575	ankyrin 3, long sp
25	127.5	16.8	1786	2 A57282	ankyrin-related pr
26	127.5	16.8	1815	2 T15346	ankyrin-related pr
27	127.5	16.8	1867	2 T15346	ankyrin-related pr
28	127.5	16.8	2039	2 T15347	ankyrin-related un
29	126	16.6	247	2 D84448	probable ankyrin l

30	125	16.4	1964	2 T09059	notch4 - mouse
31	124.5	16.4	209	2 T15888	hypothetical prote
32	121	15.9	237	2 T50984	related to 265 pro
33	121	15.9	888	2 D84650	probable potassium
34	120	15.8	476	2 T23213	hypothetical prote
35	118.5	15.6	347	2 C40858	GA-binding protein
36	118.5	15.6	382	2 B40858	GA-binding protein
37	117.5	15.5	347	2 C48146	nuclear respirator
38	117.5	15.5	348	2 I38744	nuclear respirator
39	117.5	15.5	360	2 I38743	nuclear respirator
40	117.5	15.5	395	2 I38741	nuclear respirator
41	117	15.4	1435	2 T32930	hypothetical prote
42	116	15.3	1549	2 T13940	ankyrin - fruit fl
43	115.5	15.2	1058	2 D82654	ankyrin-like prote
44	114	15.0	828	2 T52046	potassium channel
45	114	15.0	2437	2 S42612	transmembrane prot

#### ALIGNMENTS

RESULT 1  
JE0141  
cyclin dependent kinase inhibitor - human  
N:Alternate names: CDK4 inhibitor p16(INK4A/MTS1); cyclin-dependent kinase inhibitor  
C:Species: Homo sapiens (man)  
C>Date: 02-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 19-May-2000  
C:Accession: JE0141; I59268; S39359; I59585; J05679  
R:Huang, C.G.; Deng, W.; Fu, J.L.  
Chin, J. Biotechnol 13, 105-107, 1997  
A:Title: Molecular cloning and sequencing of p16 ink4 cDNA from hela cell.  
A:Reference number: JE0141  
A:Accession: JE0141  
A:Molecule type: mRNA  
A:Residues: 1-156 <HUA>  
A:Experimental source: Hella cell  
R:Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagihara, K.; Hussain, S.P.; Bennett, proc. Natl. Acad. Sci. U.S.A. 91, 11045-11049, 1994  
A:Title: Mutations and altered expression of p16INK4 in human cancer.  
A:Reference number: I59268; M01D:95062202  
A:Accession: I59268  
A>Status: translation not shown; translated from GB/EHML/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-152 <OKA>  
A:Cross-references: GB:I27211; NID:9558656; PIDN:AA92554.1; PID:9558657  
A:Note: the sequence is revised in GenBank entry HUMINK4X, release 113.0, PIDN:AA925  
R:Serrano, M.; Hannon, G.J.; Beach, D.  
Nature 366, 704-707, 1993  
A:Title: A new regulatory motif in cell-cycle control causing specific inhibition of  
A:Reference number: S39359; M01D:94081956  
A:Accession: S39359  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 9-34, 'V', 36-156 <SER>  
A:Note: This sequence is corrected in reference I59268  
R:Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.; Science 264, 436-440, 1994  
A:Title: A cell cycle regulator potentially involved in genesis of many tumor types.  
A:Reference number: I59585; M01D:94204645  
A:Accession: I59585  
A>Status: translation not shown; translated from GB/EHML/DBDJ  
A:Molecule type: DNA  
A:Residues: 51-152 <KAM>  
A:Cross-references: GB:S69804; NID:9546272; PIDN:AA014048.1; PID:94261748  
C:Comment: This protein inhibits the activity of cyclin D1/CDK4 and cyclin D1/CDK6 k1  
C:Genetics:  
A:Gene: GDB:CDKN2A; CDK4I; MCM; P16; INK4; MTS1; CMM2; CDKN2  
A:Cross-references: GDB:335362; OMIM:600160  
A:Map position: 9p21-9p21  
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol  
C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

Query Match 99.1%; Score 753; DB 2; Length 156;  
 Best Local Similarity 99.3%; Pred. No. 1.3e-64;  
 Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MEPSADMLATAAARGVEEVALLEAVLPAAPNSYGRPRIOVMMGSAVAELLILHGA 60  
 |||||  
 Db 9 MEPSADMLATAAARGVEEVALLEAGALPAPNSYGRPRIOVMMGSAVAELLILHGA 68  
 |||||  
 OY 61 EPNCDPATLTPVPAHAREGFLDTLVVLRAGARLDVARDAGRLPVDLAEEELGHRDVAR 120  
 |||||  
 Db 69 EPNCDPATLTPVPAHAREGFLDTLVVLRAGARLDVARDAGRLPVDLAEEELGHRDVAR 128  
 |||||  
 OY 121 YLRAAAGTSGSNHARIDAEPSDIPD 148  
 |||||  
 Db 129 YLRAAAGTSGSNHARIDAEPSDIPD 156  
 |||||

RESULT 2  
 178845  
 p15INK4b - mouse  
 Species: Mus sp. (mouse)  
 Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 19-May-2000  
 C:Accession: I78845

R:Quelle: D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.; W  
 Oncogene 11, 635-645, 1995  
 A:Title: Cloning and characterization of murine p15INK4a and p15INK4b genes.

A:Reference number: 158352; MUID:95380169  
 A:Accession: 178845  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-130 <RES>  
 A:Cross-references: GB:S79252; NID:q1087092; PID:q1087093  
 C:Gene: p15INK4b  
 C:Genetics:  
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

Query Match 69.6%; Score 529; DB 2; Length 130;  
 Best Local Similarity 88.3%; Pred. No. 2.4e-43;  
 Matches 106; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 8 LATAAARGVEEVALLEAVLPAAPNSYGRPRIOVMMGSAVAELLILHGAEPNCADP 67  
 |||||  
 Db 10 LATAAARGVEEVALLEAGADPNALNFRGRPRIOVMMGSAVAELLILHGAEPNCADP 69  
 |||||  
 OY 68 ATLTPRVHAAAREGFLDTLVVLRAGARLDVARDAGRLPVDLAEEELGHRDVAR 127  
 |||||  
 Db 70 ATLTPRVHAAAREGFLDTLVVLRAGARLDVARDAGRLPVDLAEEELGHRDVAR 129  
 |||||

CDK4 inhibitor p14(INK4B/MTS2) - human  
 N:Alternate names: CDK6-associated protein p15(INK4b); cyclin-dependent kinase inhibitor  
 C:Species: Homo sapiens (man)  
 C:Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 21-Jul-2000  
 C:Accession: B55479; S47593; I81183; I52713  
 R:Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.;  
 Genes Dev. 8, 2939-2952, 1994  
 A:Title: Growth suppression by p18, a p16(INK4/MTS1) and p14(INK4B/MTS2)-related CDK6  
 A:Reference number: A55479; MUID:95095079  
 A:Accession: B55479  
 A:Molecule type: mRNA  
 A:Residues: 1-138 <GUA>  
 A:Cross-references: GB:U17075; NID:9639715; PIDN:AA50075.1; PID:9639716  
 A:Experimental source: HeLa cells  
 R:Hannon, G.J.; Beach, D.  
 Nature 371, 257-261, 1994  
 A:Title: p15(INK4B) is a potential effector of TGF-beta-induced cell cycle arrest.  
 A:Reference number: S47593; MUID:94359613  
 A:Accession: S47593  
 A:Molecule type: mRNA  
 A:Residues: 1-119, 'TP', 22, 24-31, 'HSW', 35-138 <HAN>

A:Cross-references: GB:I36844; NID:9556197; PIDN:AA50282.1; PID:9556198  
 A:Experimental source: Hacat cells  
 R:Ham, A.; Grusis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Hartsman, K.; Tavtigian, S.V.;  
 Science 264, 436-440, 1994  
 A:Title: A cell cycle regulator potentially involved in genesis of many tumor types.  
 A:Reference number: I59585; MUID:94204645  
 A:Accession: I81183

A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 53-138 <KAN>  
 A:Cross-references: GB:S69805; NID:9546273; PIDN:AA14049.1; PID:94261749  
 R:Gen, J.; Harper, J.W.; Bigner, S.H.; Bigner, D.D.; Papadopoulos, N.; Markowitz, S.;  
 Cancer Res. 54, 6353-6358, 1994  
 A:Title: Deletion of p16 and p15 genes in brain tumors.

A:Reference number: I52713; MUID:95079408  
 A:Accession: I52713  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-52 <RES>  
 A:Cross-references: GB:S75756; NID:9861470; PIDN:AA14186.1; PID:94261886  
 C:Gene: p15INK4b  
 C:Genetics:  
 A:Gene: GDB:CDKN2B; MTS2  
 A:Cross-references: GDB:S79577; OMIM:600431  
 A:Map position: 9p21-9p21  
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol  
 C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

Query Match 68.7%; Score 522; DB 2; Length 138;  
 Best Local Similarity 85.5%; Pred. No. 1.2e-42;  
 Matches 106; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

OY 4 SADMLATAAARGVEEVALLEAVLPAAPNSYGRPRIOVMMGSAVAELLILHGAEPN 63  
 |||||  
 Db 14 SDESLAAARGVEEVALLEAGADPNNGVNGRRRAIOVMMGSAVAELLILHGAEPN 73  
 |||||  
 OY 64 CADPATLTPRVHAAAREGFLDTLVVLRAGARLDVARDAGRLPVDLAEEELGHRDVAR 123  
 |||||  
 Db 74 CADPATLTPRVHAAAREGFLDTLVVLRAGARLDVARDAGRLPVDLAEEELGHRDVAR 133  
 |||||  
 OY 124 AAAG 127  
 |||||  
 Db 134 TATG 137  
 |||||

RESULT 4  
 158352  
 p16INK4a - mouse  
 Species: Mus sp. (mouse)  
 C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 24-Nov-1999  
 C:Accession: I58352  
 R:Quelle: D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.;  
 Oncogene 11, 635-645, 1995  
 A:Title: Cloning and characterization of murine p16INK4a and p15INK4b genes.  
 A:Reference number: I58352; MUID:95380169  
 A:Accession: I58352  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-167 <RES>  
 A:Cross-references: GB:S79251; NID:q1087090; PID:q1087091  
 C:Gene: p16INK4a  
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol

Query Match 60.7%; Score 461.5; DB 2; Length 167;  
 Best Local Similarity 63.2%; Pred. No. 8.5e-37;  
 Matches 98; Conservative 16; Mismatches 32; Indels 9; Gaps 3;

OY 1 MEPSADMLATAAARGVEEVALLEAVLPAAPNSYGRPRIOVMMGSAVAELLILHGA 60  
 |||||  
 Db 1 MESADRLA-RAAGRVHDAAREGFLDTLVVLRAGARLDVARDAGRLPVDLAEEELGHRDVAR 59  
 |||||



[illegible]

DB 1 MMGSAQVAEILLHGCAPNCADPATLTRPVHADAREGFLD 41

RESULT 11  
537431  
ankyrin 2, neuronal long splice form - human  
N:Alternate names: ankyrin B, 440K splice form; ankyrin-B, brain ankyrin; non-erythro  
N:Contains: ankyrin 2, short form  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 13-Aug-1999  
C:Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569  
R:Chan, W.  
submitted to the EMBL Data Library, September 1993  
A:Reference number: S37431  
A:Accession: S37431  
A:Accession: S37431  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-3924 <CHA>  
A:Cross-references: EMBL:Z26634; NID:9406287; PIDN:CAA81387.1; PID:9406288  
R:Otto, E.; Kunitomo, M.; McLaughlin, T.; Bennett, V.  
J. Cell Biol. 114, 241-253, 1991  
A:Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal  
A:Reference number: A39643; MUID:91302466  
A:Accession: A39643  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1443,3585-3924 <OIT>  
A:Cross-references: EMBL:X56958  
R:Itse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Wa  
Germos 10, 858-866, 1991  
A:Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.  
A:Reference number: A40334; MUID:92009921  
A:Accession: A40334  
A:Molecule type: DNA  
A:Residues: 463-474,'PE',477-495 <TSE>  
A:Cross-references: GB:M31123; NID:9178647; PIDN:AAA62828.1; PID:9178648  
R:Chan, W.; Kortell, E.; Bennett, V.  
J. Cell Biol. 123, 1463-1473, 1993  
A:Title: 440-kD ankyrinB: structure of the major developmentally regulated domain and  
A:Reference number: A49462; MUID:94075409  
A:Accession: A49462  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-3324 <RSS>  
A:Cross-references: EMBL:Z26634; NID:9406287; PIDN:CAA81387.1; PID:9406288  
C:Genetics:  
A:Gene: GDB:ANK2  
A:Cross-references: GDB:127607; OMIM:106410  
A:Map position: 4q25-4q27  
C:Superfamily: ankyrin, ankyrin repeat homology  
C:Keywords: alternative splicing  
F:2-3924/Product: ankyrin 2, long form #status predicted <MAT>  
F:2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MA>  
F:63-95/Domain: ankyrin repeat homology <AN01>  
F:96-128/Domain: ankyrin repeat homology <AN02>  
F:129-161/Domain: ankyrin repeat homology <AN03>  
F:162-190/Domain: ankyrin repeat homology <AN04>  
F:191-223/Domain: ankyrin repeat homology <AN05>  
F:232-264/Domain: ankyrin repeat homology <AN06>  
F:265-297/Domain: ankyrin repeat homology <AN07>  
F:298-330/Domain: ankyrin repeat homology <AN08>  
F:331-363/Domain: ankyrin repeat homology <AN09>  
F:364-396/Domain: ankyrin repeat homology <AN10>  
F:397-429/Domain: ankyrin repeat homology <AN11>  
F:430-462/Domain: ankyrin repeat homology <AN12>  
F:463-495/Domain: ankyrin repeat homology <AN13>  
F:496-528/Domain: ankyrin repeat homology <AN14>  
F:529-561/Domain: ankyrin repeat homology <AN15>





**RESULT 14**

B35049  
ankyrin 1, erythrocyte splice form 3 - human  
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R  
N:Contains: ankyrin 2.2, erythrocyte  
C:Species: Homo sapiens (man)  
C>Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 10-Jul-1998  
C:Accession: B35049  
R:Lambert, S.; Yu, H.: Prechal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; R:  
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990  
A:Title: cDNA sequence for human erythrocyte ankyrin.  
A:Reference number: A35049; MUID:90175370  
F:Accession: B35049  
A>Status: preliminary  
A:Molecule type: mRNA  
C:Genetics:  
A:Residues: 1-1856 <LAMB>  
A:Gene: GDB:ANK1; ANK  
A:Cross-references: GDB:118737; OMIM:182900  
Map position: Rp11.2-Rp11.2  
Superfamily: ankyrin; ankyrin repeat homology  
Keywords: alternative splicing  
F:2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MA1>  
F:2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>  
F:44-76/Domain: ankyrin repeat homology <AN01>  
F:77-109/Domain: ankyrin repeat homology <AN02>  
F:110-142/Domain: ankyrin repeat homology <AN03>  
F:143-171/Domain: ankyrin repeat homology <AN04>  
F:172-204/Domain: ankyrin repeat homology <AN05>  
F:205-237/Domain: ankyrin repeat homology <AN06>  
F:238-270/Domain: ankyrin repeat homology <AN07>  
F:271-303/Domain: ankyrin repeat homology <AN08>  
F:304-336/Domain: ankyrin repeat homology <AN09>  
F:337-369/Domain: ankyrin repeat homology <AN10>  
F:370-402/Domain: ankyrin repeat homology <AN11>  
F:403-435/Domain: ankyrin repeat homology <AN12>  
F:436-468/Domain: ankyrin repeat homology <AN13>  
F:469-501/Domain: ankyrin repeat homology <AN14>  
F:502-534/Domain: ankyrin repeat homology <AN15>  
F:535-567/Domain: ankyrin repeat homology <AN16>  
F:568-600/Domain: ankyrin repeat homology <AN17>  
F:601-633/Domain: ankyrin repeat homology <AN18>  
F:634-666/Domain: ankyrin repeat homology <AN19>  
F:667-699/Domain: ankyrin repeat homology <AN20>  
F:700-732/Domain: ankyrin repeat homology <AN21>  
F:733-765/Domain: ankyrin repeat homology <AN22>  
F:766-798/Domain: ankyrin repeat homology <AN23>

**Nery Match** 17.6%; Score 133.5; DB 2; Length 1856;  
Best Local Similarity 35.4%; Pred. No. 0.00023;  
Matches 52; Conservative 15; Mismatches 29; Indels 11; Gaps 6;

OY 8 LATAAGRVEEVRALLDAVALPNAPNSYGRRPIOV-MMMGSARYAEILLHGAEPCAD 66  
| | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 507 LHIAAREGHVETVLLLEKEASQACMTKKGFTPLHVAAYKGVRVAELLERDAPNAAG 566  
| | | | | | | | | | | | | | | | | | | | | | | | | | |  
OY 67 PATLRPRVNDARSEFLDTL-VYLHRAGARDLVRAW-GRLPVDLAELGGHDVARYL-- 122  
| | | | | | | : : : | | : | | | | | | | | | | | | | | |  
Db 567 KNGLT-PLTHVAHHNNLLIVKLRLPRGS--PHSPAMMGYPPLHTAAKONOVEAVARSILQ 623  
| | | | | | | : : | | : | | | | | | | | | | | | | | |  
OY 123 --RAAAGTRGSHARIDAAEGPSDI 146  
| | | | | | | : | | : | | | | | | | | | | | | | | | |  
Db 624 YGGSANAESYGVPTPLHLAAGCGHAEM 650

**RESULT 15**  
A35049  
ankyrin 1' erythrocyte splice form 2 - human  
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R  
N:Contains: Homo sapiens (man)

```
C>Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 04-Sep-1998
C:Accession: A35049
C:Rilambert, S.; Yu, H.; Pechal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
A>Title: cDNA sequence for human erythrocyte ankryrin.
A:Reference number: A35049; MUID:90157370
A:Accession: A35049
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1880 <LAM>
A:Cross-references: GB:M28880
C:Genetics:
A:Gene: GDB:ANK1; ANK
A:Cross-references: GDB:118737; OMIM:182900
A:Map position: bp11.2-bp11.2
C:Superfamily: ankryrin; ankryrin repeat homology
C:Keywords: alternative splicing; cytoskeleton
F:2-1880/Product: ankryrin 1, erythrocyte form 2 #status predicted <MAT>
F:2-1513/1676-1880/Product: ankryrin 2.2, erythrocyte #status predicted <MA2>
F:44-76/Domain: ankryrin repeat homology <AN01>
F:77-109/Domain: ankryrin repeat homology <AN02>
F:110-142/Domain: ankryrin repeat homology <AN03>
F:143-171/Domain: ankryrin repeat homology <AN04>
F:172-204/Domain: ankryrin repeat homology <AN05>
F:205-237/Domain: ankryrin repeat homology <AN06>
F:238-270/Domain: ankryrin repeat homology <AN07>
F:271-303/Domain: ankryrin repeat homology <AN08>
F:304-336/Domain: ankryrin repeat homology <AN09>
F:337-369/Domain: ankryrin repeat homology <AN10>
F:370-402/Domain: ankryrin repeat homology <AN11>
F:403-435/Domain: ankryrin repeat homology <AN12>
F:436-468/Domain: ankryrin repeat homology <AN13>
F:469-501/Domain: ankryrin repeat homology <AN14>
F:502-534/Domain: ankryrin repeat homology <AN15>
F:535-567/Domain: ankryrin repeat homology <AN16>
F:568-600/Domain: ankryrin repeat homology <AN17>
F:601-633/Domain: ankryrin repeat homology <AN18>
F:634-666/Domain: ankryrin repeat homology <AN19>
F:667-699/Domain: ankryrin repeat homology <AN20>
F:700-733/Domain: ankryrin repeat homology <AN21>
F:733-765/Domain: ankryrin repeat homology <AN22>
F:766-798/Domain: ankryrin repeat homology <AN23>
```

Search completed: September 19, 2002, 17:24:24  
Job time: 83 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:23:41 ; Search time 11.84 Seconds

(without alignments)  
483.994 Million cell updates/sec

Title: US-09-016-869b-35

Perfect score: 760

Sequence: 1 MEPSADWLATAAARGRVEFV.....TRGSNHRIDAAGPSDIPD 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	753	99.1	156	1	CDN2_HUMAN
2	529	69.6	130	1	CDN5_MOUSE
3	524	68.9	130	1	CDN5_RAT
4	522	68.7	138	1	CDN5_HUMAN
5	461.5	60.7	167	1	CDN2_MOUSE
6	408	53.7	171	1	CDN2_MONDO
7	259	34.1	166	1	CDN7_HUMAN
8	249	32.8	166	1	CDN7_MOUSE
9	231.5	30.5	168	1	CDN6_MOUSE
10	228.5	30.1	168	1	CDN6_HUMAN
11	158	20.8	3924	1	ANK2_HUMAN
12	137.5	18.1	1862	1	ANK2_MOUSE
13	133.5	17.6	768	1	YB23_HUMAN
14	133.5	17.6	1880	1	ANK1_HUMAN
15	130.5	17.2	1431	1	DAPK_HUMAN
16	125	16.4	1964	1	NTCA_MOUSE
17	123	16.2	1059	1	Y379_HUMAN
18	118.5	15.6	347	1	GABG_MOUSE
19	118.5	15.6	382	1	GABG_MOUSE
20	117.5	15.5	347	1	GABG_HUMAN
21	117.5	15.5	383	1	GABG_HUMAN
22	114	15.0	768	1	BARI_RAT
23	114	15.0	2437	1	NOMC_BRARE
24	113	14.9	437	1	V014_FOWPV
25	111.5	14.7	2531	1	NTC1_RAT
26	111	14.6	777	1	ANKH_CHRVI
27	111	14.6	333	1	BARI_HUMAN
28	110.5	14.5	2444	1	NTC1_HUMAN
29	109.5	14.4	832	1	ANKR_HUMAN
30	107.5	14.1	592	1	V246_FOWPV
31	107	14.1	765	1	BARI_MOUSE
32	106.5	14.0	2703	1	NOMC_MOUSE
33	104.5	13.8	2524	1	NOMC_XENLA

34	103.5	13.6	2318	1	NTC3_MOUSE	061982 mus musculus
35	102.5	13.5	740	1	Y050_HUMAN	015027 homo sapien
36	100.5	13.2	414	1	GABD_MOUSE	P81069 mus musculus
37	100.5	13.2	500	1	CACT_DROME	003017 mus musculus
38	100.5	13.2	1178	1	PHB1_YEAST	P17442 saccharomyc
39	100	13.2	668	1	V244_FOWPV	091426 fowlpox vir
40	99.5	13.1	1454	1	KDGE_DROME	009103 drosophila
41	98	12.9	708	1	G1T2_MOUSE	091192 mus musculus
42	96.5	12.7	461	1	V218_FOWPV	093517 fowlpox vir
43	96.5	12.7	605	1	GLS1_CAEL	019013 caenorhabdi
44	96	12.6	603	1	V162_FOWPV	091569 fowlpox vir
45	96	12.6	735	1	RMSA_MOUSE	005921 mus musculus

## ALIGNMENTS

RESULT	ID	CDN2_HUMAN	STANDARD	PRT	156 AA.
AC	P42771	O15191			
DT	01-NOV-1995	(Rel. 32, Created)			
DT	15-JUL-1998	(Rel. 36, Last sequence update)			
DT	01-MAR-2002	(Rel. 41, Last annotation update)			
DE	Cyclin-dependent kinase 4 inhibitor A (CDK4) (P16-INK4) (P16-INK4A)				
DE	(Multiple tumor suppressor 1) (MTS1).				
GN	CDKN2A OR CDKN2.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI-TaxID=9606;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=94081956; PubMed=8259215;				
RT	Serrano M., Hannon G.J., Beach D.;				
RT	"A new regulatory motif in cell-cycle control causing specific				
RT	inhibition of cyclin D/CDK4."				
RL	Nature 366:704-707(1993).				
RN	(2)				
RP	SEQUENCE OF 51-152 FROM N.A.				
RA	MEDLINE=94204645; PubMed=8153634;				
RA	Kamb A., Grus N.A., Weaver-Feldhaus J., Liu Q., Harsman K.,				
RA	Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,				
RT	Skolnick M.H.;				
RT	"A cell cycle regulator potentially involved in genesis of many tumor				
RT	types."				
RL	Science 264:436-440(1994).				
RN	(3)				
RP	SEQUENCE OF 1-20 FROM N.A.				
RA	MEDLINE=96182088; PubMed=8622687;				
RA	Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;				
RT	"Regulation of p16CDKN2 expression and its implications for cell				
RT	immortalization and senescence."				
RL	Mol. Cell. Biol. 16:859-867(1996).				
RN	(4)				
RP	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.				
RA	MEDLINE=98421670; PubMed=9751050;				
RA	Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;				
RT	"Structural basis for inhibition of the cyclin-dependent kinase Cdk6				
RT	by the tumour suppressor p16INK4a."				
RL	Nature 395:237-243(1998).				
RN	(5)				
RP	STRUCTURE BY NMR.				
RA	MEDLINE=20027100; PubMed=10559205;				
RA	Yuan C., Li J., Selby T.L., Byeon I.J., Tsai M.D.;				
RT	"Tumor suppressor INK4: comparisons of conformational properties				
RT	between p16(INK4a) and p18(INK4C)."				
RL	J. Mol. Biol. 294:201-211(1999).				
RN	(6)				
RP	REVIEW ON MELANOMA VARIANTS.				
RA	MEDLINE=96377761; PubMed=8783570;				
RA	Dracopoli N.C., Fountain J.W.;				
RT	"CDKN2 mutations in melanoma."				

RL Cancer Surv. 26:115-132(1996).  
 RN [7]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=96303699; PubMed=8723678;  
 RA Smit-Saunders B., Hovig E.;  
 RT "CDKN2A (p16INK4A) somatic and germline mutations.";  
 RL Hum. Mutat. 7:294-303(1996).  
 RN [8]  
 RP VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).  
 RX MEDLINE=94338323; PubMed=8060323;  
 RA Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;  
 RT "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41  
 (cyclin-dependent kinase-4 inhibitor) gene in human primary non-small  
 cell lung carcinomas.";  
 RL Biochem. Biophys. Res. Commun. 202:1426-1430(1994).  
 RN [9]  
 RP VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 AND  
 RX THR-148.  
 RX MEDLINE=95078916; PubMed=7987387;  
 RA Hussussian C.J., Struwing J.P., Goldstein A.M., Haggins P.A.T.,  
 Ally D.S., Sheehan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.;  
 RT "Germline p16 mutations in familial melanoma.";  
 RL Nat. Genet. 8:15-21(1994).  
 RN [10]  
 RP VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.  
 RX MEDLINE=95060835; PubMed=7970734;  
 RA Zhou X., Tarrin L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,  
 RA Abraham J.M., Meltzer S.J.;  
 RT "The MTS1 gene is frequently mutated in primary human esophageal  
 tumors.";  
 RL Oncogene 9:3737-3741(1994).  
 RN [11]  
 RP VARIANTS.  
 RX MEDLINE=95188190; PubMed=7882351;  
 RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,  
 RA Demetree D.J., Serrano M., Hannon G.J., Shiseki M., Zarivala M.,  
 RA Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.;  
 RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in  
 primary and metastatic lung cancer.";  
 RL Cancer Res. 55:1448-1451(1995).  
 RN [12]  
 RP VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.  
 RX MEDLINE=96121580; PubMed=8595405;  
 RA Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M.,  
 RA Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;  
 RT "Mutations of the CDKN2/p16INK4 gene in Australian melanoma  
 kindreds.";  
 RL Hum. Mol. Genet. 4:1845-1852(1995).  
 RN [13]  
 RP CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 AND  
 T-148.  
 RX MEDLINE=95375774; PubMed=7647780;  
 RA Renade K., Hussussian C.J., Sikorski R.S., Varmus H.E.,  
 RA Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,  
 RA Dracopoli N.C.;  
 RT "Mutations associated with familial melanoma impair p16INK4  
 function.";  
 RL Nat. Genet. 10:114-116(1995).  
 RN [14]  
 RP VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68, T-85 AND T-148.  
 RX MEDLINE=96323259; PubMed=8710906;  
 RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,  
 RA Lucchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,  
 RA Iselbacher K.J., Sober A.J., Haber D.A.;  
 RT "Prevalence of germ-line mutations in p16, p19ARF, and CDK4 in  
 familial melanoma: analysis of a clinic-based population.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).  
 RN [15]  
 RP VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.  
 RX MEDLINE=97472457; PubMed=9328469;  
 RA Harland M., Meloni R., Gruis N., Pinney E., Brookes S., Spurr N.K.,  
 RA Fritschauf A.-M., Battaille V., Peters G., Cuzick J., Selby P.,  
 RA Bishop D.J., Bishop J.N.;

RT "Germline mutations of the CDKN2 gene in UK melanoma families.";  
 RL Hum. Mol. Genet. 6:2061-2067(1997).  
 RN [16]  
 RP VARIANTS FAMILIAL MELANOMA.  
 RX MEDLINE=96087572; PubMed=9425228;  
 RA Soulier N., Avril M.-F., Chompret A., Demenais F., Bombléd J.,  
 RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-de Pallieres B.;  
 RT "Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone  
 families in France.";  
 RL Hum. Mol. Genet. 7:209-216(1998).  
 RN [17]  
 RP ERRATUM.  
 RA Soulier N., Avril M.-F., Chompret A., Demenais F., Bombléd J.,  
 RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-de Pallieres B.;  
 RL Hum. Mol. Genet. 7:941-941(1998).  
 RN [18]  
 RP VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.  
 RA Greisdorf S., Olafsdottir G.H., Borg A.;  
 RT "Five novel somatic CDKN2/p16 mutations identified in melanoma,  
 RT glioma and carcinoma of the pancreas.";  
 RL Hum. Mutat. 12:212-212(1998).  
 RN [19]  
 RP VARIANTS MELANOMA GLY-59; TYR-84; TRP-87 AND TRP-101.  
 RX MEDLINE=20332815; PubMed=10874641;  
 RA Ruiz A., Pulig S., Malvey J., Lazaro C., Lynch M., Gimenez-Arnau A.M.,  
 RA Pulig L., Sanchez-Conejero J., Estivill X., Castel T.;  
 RT "CDKN2A mutations in Spanish cutaneous malignant melanoma families and  
 RT patients with multiple melanomas and other neoplasia.";  
 RL J. Med. Genet. 36:480-493(1999).  
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS  
 CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE  
 CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.  
 CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.  
 CC -1- DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A  
 CC WIDE RANGE OF TISSUES.  
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
 CC INHIBITORS.  
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.  
 CC -----  
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 CC -----  
 DR EMBL: L27211; AAA92554.1; -;  
 DR EMBL: U12820; AAB60645.1; -;  
 DR EMBL: U12819; AAB60645.1; JOINED.  
 DR EMBL: U12819; AAB60645.1; JOINED.  
 DR EMBL: S69804; AAD14048.1; -;  
 DR EMBL: X94154; CAA63870.1; -;  
 DR PDB: 1B17; 16-FEB-99.  
 DR PDB: 1DC2; 23-DEC-99.  
 DR MIM: 600160; -;  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 3.  
 DR PROSITE: PS50088; ANK\_REPEAT; FALSE\_NEG.  
 DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
 KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;  
 KW Polymorphism; Li-Fraumeni syndrome; 3D-structure.  
 FT REPEAT 11 40 ANK 1.  
 FT REPEAT 44 72 ANK 2.  
 FT REPEAT 77 106 ANK 3.  
 FT REPEAT 110 139 ANK 4.  
 FT REPEAT 14 14 ANK 4.  
 FT VARIANT D->E (IN A BILARY TRACT TUMOR).  
 FT /FTid=VAR\_001408.  
 FT VARIANT 16 16 L->P (IN A BILARY TRACT TUMOR AND A  
 FT FAMILIAL MELANOMA).  
 FT /FTid=VAR\_001409.  
 FT A->P (IN A LUNG TUMOR AND MELANOMA).  
 FT /FTid=VAR\_001410.

Query Match 99.1%; Score 753; DB 1; Length 156;  
 Best Local Similarity 99.3%; Pred. No. 1.2e-65;  
 Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESSAWMLTAARGRVEEVRALLEVALPNNAPNSYGRPRIOVMMGSAVVAELLILHGA 60  
 DB 9 MESSAWMLTAARGRVEEVRALLEVALPNNAPNSYGRPRIOVMMGSAVVAELLILHGA 68

QY 61 EPNACADPATITRPVHDAAREGFLDTLVLRAGARLDVDCAMGRPLPVDLAEEIGHRDVAR 120  
 DB 69 EPNACADPATITRPVHDAAREGFLDTLVLRAGARLDVDCAMGRPLPVDLAEEIGHRDVAR 128

QY 121 YLRAAAGTRGSHNARIIDAAEGPSDIPD 148  
 DB 129 YLRAAAGTRGSHNARIIDAAEGPSDIPD 156

RESULT 2  
 QY MOUSE STANDARD; PRT; 130 AA.  
 AC P55271;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cyclin-dependent kinase 4 inhibitor B (P14-INK4B) (P15-INK4B).  
 GN CDKN2B.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95380169; PubMed=7651726;  
 RA Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,  
 RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;  
 RT Cloning and characterization of murine p16INK4a and p15INK4b genes.;  
 RL Oncogene 11:635-645(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6J X DBA;  
 RA MEDLINE=97322242; PubMed=9178896;  
 RA Melumbres M., de Castro I., Santos J., Melendez B., Mangues R.,  
 RA Serrano M., Pellicer A., Fernandez-Piqueras J.;  
 RT Inactivation of the cyclin-dependent kinase inhibitor p15INK4b by  
 RT deletion and de novo methylation with independence of p16INK4a  
 RT alterations in murine primary T-cell lymphomas.;  
 RI Oncogene 14:1361-1370(1997).  
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.  
 CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY  
 CC SIMILARITY).  
 CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED UBICUOUSLY.  
 CC -1- INDUCTION: BY TGF-BETA.  
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
 CC INHIBITORS.  
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.  
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 CC -----  
 DR EMBL: U66085; AAB39833.1;  
 DR EMBL: U66084; AAB39833.1; JOINED.  
 DR HSSP: P42771; 1B17.  
 DR MGD: MGI:104737; Cdkn2b.  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank.3.  
 DR SMART: SM00248; ANK.1.

DR PROSITE; PSS0088; ANK\_REPEAT. 1.  
 DR PROSITE; PSS0297; ANK\_REPEAT\_REGION. 1.  
 KW Cell Cycle; Anti-oncogene; Repeat; ANK repeat.  
 FT REPEAT 5 34 ANK 1.  
 FT REPEAT 38 66 ANK 2.  
 FT REPEAT 71 100 ANK 3.  
 FT REPEAT 104 130 ANK 4.  
 SQ SEQUENCE 130 AA; 1378 MW; 7AAD60FF52BCFP9 CRC64;

Query Match 69.6%; Score 529; DB 1; Length 130;  
 Best Local Similarity 88.3%; Pred. No. 3.4e-44;  
 Matches 106; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 8 LATAARGRVEEVRALLEVALPNNAPNSYGRPRIOVMMGSAVVAELLILHGAEPNCADP 67  
 DB 10 LATAARGRVEEVRALLEVALPNNAPNSYGRPRIOVMMGSAVVAELLILHGAEPNCADP 69

QY 68 ATLTPRVHDAAREGFLDTLVLRAGARLDVDCAMGRPLPVDLAEEIGHRDVAR 127  
 DB 70 ATLTPRVHDAAREGFLDTLVLRAGARLDVDCAMGRPLPVDLAEEIGHRDVAR 129

RESULT 3  
 QY CDKN2\_RAT STANDARD; PRT; 130 AA.  
 AC P55272;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cyclin-dependent kinase 4 inhibitor B (P14-INK4B) (P15-INK4B).  
 GN CDKN2B OR INK4.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96001392; PubMed=7546221;  
 RA Hino O., Kobayashi E., Hirayama Y., Kubo Y.,  
 RA Tsuchiya H., Kikuchi Y., Mitani H.;  
 RT Molecular genetic basis of renal carcinogenesis in the Eker rat  
 RT model of tubercular sclerosis (Tsc2).;  
 RL Mol. Carcinog. 14:23-27(1995).  
 RN [2]  
 RP SEQUENCE OF 46-86 FROM N.A.  
 RX MEDLINE=95228036; PubMed=7712460;  
 RA Knapek D.F., Serrano M., Beach D., Trono D., Walker C.L.;  
 RT Association of rat p15INK4B/p16INK4 deletions with monosomy 5 in  
 RT kidney epithelial cell lines but not primary renal tumors.;  
 RL Cancer Res. 55:1607-1612(1995).  
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.  
 CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY  
 CC SIMILARITY).  
 CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4.  
 CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE  
 CC INITIATION CODONS IN THE SAME READING FRAME.  
 CC -1- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN  
 CC TESTIS, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL  
 CC KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.  
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
 CC INHIBITORS.  
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.  
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 CC -----  
 DR EMBL: S79760; AAB35360.1; .

DR EMBL: S77734; -. NOT\_ANNOTATED\_CD5.  
 DR HSSP: Q60773; IAP7.  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 3.  
 DR SMART: SM00248; ANK; 1.  
 DR PROSITE: PSS0088; ANK\_REPEAT; 1.  
 DR PROSITE: PSS0297; ANK\_REPEAT\_REGION; 1.  
 DR Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.  
 FT CHAIN 1 130  
 FT CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,  
 FT LONG ISOFORM  
 FT CHAIN 46 130  
 FT CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,  
 FT SHORT ISOFORM.  
 FT INT\_MET 46 46  
 FT REPEAT 5 34  
 FT REPEAT 38 66  
 FT REPEAT 71 100  
 FT REPEAT 104 130  
 FT ANK 4.  
 SO SEQUENCE 130 AA; 13748 MW; AC45B21FA69FAD92 CRC64;

Query Match 68.9%; Score 524; DB 1; Length 130;  
 Best Local Similarity 86.7%; Pred. No. 1e-43;  
 Matches 104; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 8 LATTAAGRGVEVRALLEAVLPNAPNSYGRPIQYMMGSAVVAELLHGAEPNCADP 67  
 DB 10 LATTAAGRGVEVRALLEAVLPNAPNSYGRPIQYMMGSAVVAELLHGAEPNCADP 69  
 QY 68 ATLTPRHADARSGFDLTIVLHRAGARLDVRDAMGRPLPYDLAEELGHNDVARYLRAAG 127  
 DB 70 ATLTPRHADARSGFDLTIVLHRAGARLDVRDAMGRPLPYDLAEELGHNDVARYLRAAG 129

RESULT 4  
 ID CDNS\_HUMAN STANDARD; PRT; 138 AA.  
 AC P42772;  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cyclin-dependent kinase 4 inhibitor B (P16-INK4B) (P15-INK4B)  
 DE (Multiple tumor suppressor 2) (MTS2).  
 GN CDKN2B OR MTS2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RX MEDLINE=95095079; PubMed=8001816;  
 RA Guan K.-L., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,  
 RA Matera G.A., Xiong Y.,  
 RT "Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related  
 RT CDK6 inhibitor, correlates with wild-type p53 function."  
 RL Genes Dev. 8:2939-2952(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94359613; PubMed=8078588;  
 RA Hannon G.J., Beach D.,  
 RT "p15INK4B is a potential effector of TGF-beta-induced cell cycle  
 RT arrest."  
 RL Nature 371:257-261(1994).  
 RN [3]  
 RP SEQUENCE OF 53-138 FROM N.A.  
 RX MEDLINE=94204645; PubMed=8153634;  
 RA Kamd A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,  
 RA Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,  
 RA Skolnick M.H.,  
 RT "A cell cycle regulator potentially involved in genesis of many tumor  
 RT types".  
 RL Science 264:436-440(1994).  
 RN [4]  
 RP VARIANTS LUNG ADENOCARCINOMA GLU-47 AND VAL-50.

RX MEDLINE=95188190; PubMed=7882351;  
 RA Okamoto A., Hussain S.P., Hagihara K., Spillare E.A., Rusin M.R.,  
 RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zaitawa M.,  
 RA Xiong Y., Beach D.H., Yokota J., Harris C.C.,  
 RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in  
 RT primary and metastatic lung cancer."  
 RL Cancer Res. 55:1448-1451(1995).  
 CC -! FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.  
 CC -! POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST.  
 CC -! SUBUNIT: HETERODIMER OF P14 WITH CDK4.  
 CC -! DISEASE: CDKN2B MUTATIONS ARE INVOLVED IN TUMOR FORMATION.  
 CC -! SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
 CC INHIBITORS.  
 CC -! SIMILARITY: CONTAINS 2 ANK REPEATS.

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 -----

DR EMBL: U17075; AAC50075.1; -;  
 DR EMBL: L36844; AAA50282.1; -;  
 DR EMBL: S69805; AAD14049.1; -;  
 DR HSSP: P42771; 1B17.  
 DR MIM: 600431; -;  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 3.  
 DR PROSITE: PSS0088; ANK\_REPEAT; FALSE\_NEG.  
 DR PROSITE: PSS0297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE: PSS0297; ANK\_REPEAT\_REGION; 1.  
 KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation.  
 FT REPEAT 13 39  
 FT REPEAT 73 103  
 FT VARIANT 47 47  
 FT VARIANT 50 50  
 FT VARIANT 50 50  
 FT CONFLICT 20 21  
 FT CONFLICT 23 23  
 FT CONFLICT 32 34  
 SO SEQUENCE 138 AA; 14722 MW; 0D6FFBDA6FEAD21 CRC64;

Query Match 68.7%; Score 522; DB 1; Length 138;  
 Best Local Similarity 85.5%; Pred. No. 1.7e-43;  
 Matches 106; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 4 SADWLATTAAGRGVEVRALLEAVLPNAPNSYGRPIQYMMGSAVVAELLHGAEPN 63  
 DB 14 SDEGLASAAARGVEKRYQLLEAGADNGVRFGRRAIQYMMGSAVVAELLHGAEPN 73  
 QY 64 CADPATLTPRHADARSGFDLTIVLHRAGARLDVRDAMGRPLPYDLAEELGHNDVARYL 123  
 DB 74 CADPATLTPRHADARSGFDLTIVLHRAGARLDVRDAMGRPLPYDLAEELGHNDVAGYLR 133  
 QY 124 AAAG 127  
 DB 134 TATG 137

RESULT 5  
 ID CDN2\_MOUSE STANDARD; PRT; 167 AA.  
 AC P51480;  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cyclin-dependent kinase 4 inhibitor A (CDK4I) (P16-INK4) (P16-INK4A).  
 GN CDKN2A OR P16INK4A.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DE (Tumor suppressor CDKN2A).  
GN CDKN2A.  
OS Monodelphis domestica (Short-tailed grey opossum).  
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.  
OX NCBI\_TaxID=13616;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sherburn T.E., Gale J.M., Ley R.D.:  
RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR  
CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE  
CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).  
CC -1- SUBUNIT: HEMERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY).  
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE  
CC INITIATION CODONS IN THE SAME READING FRAME.  
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
CC INHIBITORS.  
CC -1- SIMILARITY: CONTAINS 3 ANK REPEATS.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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CC EMBL; AF064808; AAC3669.1; -  
DR EMBL; AF064808; AAC3670.1; -  
DR HSSP; P42771; 1B17.  
DR InterPro: IPR002110; ANK.  
DR Pfam; PF00023; ank; 3.  
DR PROSITE; PS50088; ANK\_REPEAT; 1.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
DR Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.  
FW CHAIN 1 171  
FT CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,  
FT LONG ISOFORM.  
FT CHAIN 35 171  
FT CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,  
FT SHORT ISOFORM.  
FT INIT\_MET 35 35  
FT REPEAT 45 74  
FT REPEAT 78 106  
FT REPEAT 111 140  
FT SEQUENCE 171 AA; 18707 MW; 694264F5D0FAF6CC CRC64;  
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Query Match 53.7%; Score 408; DB 1; Length 171;  
Best Local Similarity 69.2%; Pred. No. 2e-32;  
Matches 83; Conservative 9; Mismatches 28; Indels 0; Gaps 0;  
QY 4 SADWLATAAARGVEVEVRLLEVAVALPNAVNSYGRRIQVMMGSAVAELLILHGAEPN 63  
DB 46 SEKILTEAARGRETVVELLELGTNPNAVNFGRSAIQVMAGVRLAAILILOYGAEPN 105  
QY 64 CADPRLTRPVDAAREGLDVLVLRAGALDVRDAMGRPLPVDAEELGHRDARYLR 123  
DB 106 TPDPTTLTLPVHDAAREGLDITMLLHRGARDVDSWGRPLVDIAEQLHLYVAAYLR 165  
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RESULT 7  
CDN7\_HUMAN STANDARD; PRT; 166 AA.  
AC P55273; Q13102;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Cyclin-dependent kinase 4 inhibitor D (P19-INK4D).  
GN CDKN2D.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=96121373; PubMed=8575754;  
 RA Okuda T., Hirai H., Valentini V.A., Shurtleff S.A., Kidd V.J.,  
 RT "Molecular cloning, expression pattern, and chromosomal localization  
 of human CDKN2/p16INK4, an inhibitor of cyclin D-dependent kinases.";  
 RL Genomics 29:623-630(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Thymus;  
 RX MEDLINE=95257949; PubMed=7739548;  
 RA Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.,  
 RT "Identification of human and mouse p19, a novel CDK4 and CDK6  
 inhibitor with homology to p16INK4.";  
 RL Mol. Cell. Biol. 15:2682-2688(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96362662; PubMed=8741839;  
 RA Guan K.L., Jenkins C.W., Li Y., O'Keefe C.L., Noh S., Wu X.,  
 RT Zariwala M., Matera A.G., Xiong Y.;  
 RT "Isolation and characterization of p19INK4d, a p16-related inhibitor  
 specific to CDK6 and CDK4.";  
 RL Mol. Biol. Cell 7:57-70(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99316899; PubMed=10390011;  
 RA Newton Bishop J.A., Harland M., Bennett D.C., Battaille V.,  
 RA Goldstein A.M., Tucker M.A., Ponder B.A.J., Cuzick J., Selby P.,  
 RA Bishop D.T.;  
 RT "Mutation testing in melanoma families: INK4A, CDK4 and INK4D.";  
 RL Br. J. Cancer 80:295-300(1999).  
 RN [5]  
 RP SEQUENCE OF 1-30 FROM N.A.  
 RA Murthy S.K., Demetrick D.J.;  
 RT Submitted (Jan-1998) to the EMBL/Genbank/DBJ databases.  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.  
 RX MEDLINE=98421670; PubMed=9751050;  
 RA Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;  
 RT "Structural basis for inhibition of the cyclin-dependent kinase Cdk6  
 by the tumour suppressor p16INK4a.";  
 RL Nature 395:237-243(1998).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
 RX MEDLINE=98455510; PubMed=9782052;  
 RA Baumgartner R., Fernandez-Catalan C., Winoto A., Huber R., Engl R.A.,  
 RA Holak T.A.;  
 RT "Structure of human cyclin-dependent kinase inhibitor p19(INK4d):  
 comparison to known ankyrin-repeat-containing structures and  
 implications for the dysfunction of tumor suppressor p16(INK4a).";  
 RL Structure 6:1279-1290(1998).  
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6.  
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
 INHIBITORS.  
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: U49399; AAB03772.1; -  
 DR EMBL: U20498; AAA85436.1; -  
 DR EMBL: U40343; AAB18139.1; -  
 DR EMBL: AF061327; AAC27450.1; -  
 DR EMBL: AF044171; AAD02320.1; -  
 DR PDB: 1BI8; 16-FEB-99.  
 DR PDB: 1BD8; 14-OCT-98.

DR MM: 600927; -  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 3.  
 DR SMART: SM00248; ANK; 1.  
 DR PROSITE: PS00088; ANK\_REPEAT; 1.  
 DR PROSITE: PS0297; ANK\_REPEAT\_REGION; 1.  
 KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; 3D-structure.  
 FT REPEAT 41 69 ANK 1.  
 FT REPEAT 73 102 ANK 2.  
 FT REPEAT 106 135 ANK 3.  
 FT REPEAT 138 166 ANK 4.  
 FT CONFLICT 159 159 0 -> P (IN REF. 2).  
 SQ SEQUENCE 166 AA; 17700 MW; 2FACD11CF56340DC CRC64;  
  
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 Best Local Similarity 44.0%; Pred. No. 4e-18;  
 Matches 66; Conservative 18; Mismatches 60; Indels 6; Gaps 3;  
  
 QY 4 SADWLTAAAGRVEEVALL-EEVALPNAPNSGRPIQYMMGSAKVAEELLHGAE 62  
 DB 8 AGDRLSGAAGDVQEVRLRLHRELVHPDALNRGKTAQVMFGSTYALDELKOGASP 67  
 QY 63 NCADPATLRPVHDAAREGFLDTLVLRAGARLDVDAWGRLPVDLAEELGRDVARYL 122  
 DB 68 NVQDTSG-TSPVHDAARTGFLDTLVLRHAGADVNVDPDGALPILHLAVQEGHNAVVSFL 126  
 QY 123 RAAAG-----GTRGSNHRIDAARESPDIP 148  
 DB 127 AAESDLHRRDARGLTPLLEALQGAODLYD 156  
  
 RESULT 8  
 CDN7\_MOUSE  
 ID CDN7\_MOUSE STANDARD; PRT; 166 AA.  
 AC Q60773; Q60794; Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cyclin-dependent kinase 4 inhibitor D (p19-INK4d).  
 GN CDKN2D.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL KAPLAN;  
 RX MEDLINE=95257948; PubMed=7739547;  
 RA Hirai H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.;  
 RT "Novel INK4 proteins, p19 and p18, are specific inhibitors of the  
 cyclin D-dependent kinases CDK4 and CDK6.";  
 RL Mol. Cell. Biol. 15:2672-2681(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95257949; PubMed=7739548;  
 RA Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.,  
 RT "Identification of human and mouse p19, a novel CDK4 and CDK6  
 inhibitor with homology to p16INK4.";  
 RL Mol. Cell. Biol. 15:2682-2688(1995).  
 RN [3]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=98013176; PubMed=9353127;  
 RA Luh F.Y., Archer S.J., Domaille P.J., Smith B.O., Owen D.,  
 RA Brotherton D.H., Raine A.R., Xu X., Brizuela L., Brenner S.L.,  
 RA Laue E.D.;  
 RT "Structure of the cyclin-dependent kinase inhibitor p19INK4d.";  
 RL Nature 389:999-1003(1997).  
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6.  
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
 INHIBITORS.  
 CC -1- SIMILARITY: CONTAINS 3 ANK REPEATS.





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RX MEDLINE=96438606; PubMed=8840966;
RA Laporte J., Lachance Y., Labrie C.;
RT "A p18 mutant defective in CDK6 binding in human breast cancer
RL cells.";
RL Cancer Res. 56:4586-4589(1996).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
RX MEDLINE=98100086; PubMed=9437433;
RA Venkataraman R., Swaminathan K., Marmorstein R.;
RT "Crystal structure of the CDK4/6 inhibitory protein p18INK4c provides
RT insights into ankyrin-like repeat structure/function and
RT tumor-derived p16INK4 mutations.";
RL Nat. Struct. Biol. 5:74-81(1998).
RN [5]
RP STRUCTURE BY NMR.
RX MEDLINE=99175088; PubMed=10074345;
RA Li J., Byeon I.-J.L., Ericson K., Poi M.-J., O'Walle P., Selby T.,
RA Tsai M.-D.;
RT "Tumor suppressor INK4: determination of the solution structure of
RT p18INK4c and demonstration of the functional significance of loops in
RT p18INK4c and p16INK4A.";
RL Biochemistry 38:2930-2940(1999).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS
CC CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON
CC ENDOGENOUS RETINOBLASTOMA PROTEIN RB.
CC -1- SUBUNIT: HETERODIMER OF P18 WITH CDK6.
CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN SKELETAL MUSCLE. ALSO
CC FOUND IN PANCREAS AND HEART.
CC -1- DISEASE: CDKN2C MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
CC -----
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DR EMBL: U17074; AAC50074.1; -
DR EMBL: AF041248; AAC39782.1; -
DR EMBL: AF041250; AAC39783.1; -
DR EMBL: AF041249; AAC39783.1; JOINED.
DR PDB: 1HB; 13-JAN-99.
DR PDB: 1B09; 13-SEP-99.
DR MIM: 603369; -
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 4.
DR SMART: SM00248; ANK; 2.
DR PROSITE: PS50088; ANK_REPEAT; 2.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW Cell cycle; Repeat; ANK repeat; Disease mutation; 3D-structure.
FT REPEAT 37 65 ANK 1.
FT REPEAT 69 98 ANK 2.
FT REPEAT 102 132 ANK 3.
FT REPEAT 72 72 ANK 4.
FT VARIANT A -> P (IN BREAST CANCER; LOSS OF CDK6
FT INTERACTION).
FT FTID=VAR_001490.
SQ SEQUENCE 168 AA; 18127 MW; 5D66AFA715186E9A CRC64;

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Query Match 30.1%; Score 228.5; DB 1; Length 168;  
 Best Local Similarity 40.3%; Pred. No. 3.5e-15;  
 Matches 56; Conservative 22; Mismatches 60; Indels 1; Gaps 1;

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OY 2,EPASDLATLAARGRVEEVALLEVALPNAPNSYGRBPRIQVMMSARVALLLHGAE 61
DB 3 EPWGNELASAAARGDLEQITSLQNNVNVNANQNGFRALQYMKIGNEIARRLLRGAN 62
OY 62 PNCADPATLTRVHDAAARGFLDTLVVLRAGARLDVADANGRLPVDLAEELGHRDVAR 121

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DB 63 PDLKD-RTGFATVHDAARGFLDTLTQTLLEFQADVNIEDNGLPLHLAEGHLRVEF 121
OY 122 LRAAAGTRGSHARIDAA 140
DB 122 LVKHTASNVGHRHKKGDTA 140
RESULT 11
ID ANK2_HUMAN STANDARD; PRT; 3924 AA.
AC Q01484; Q01485;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid).
GN ANK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Brain stem;
RX MEDLINE=91302466; PubMed=1830053;
RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
RT "Isolation and characterization of cDNAs encoding human brain
RT ankyrins reveal a family of alternatively spliced genes.";
RL J. Cell Biol. 114:241-253(1991).
RN [2]
RP REVISIONS.
RA Carpenter S.;
RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain stem;
RX MEDLINE=94075409; PubMed=8253844;
RA Chan W., Kordeli E., Bennett V.;
RT "440-kD ankyrin: structure of the major developmentally regulated
RT domain and selective localization in unmyelinated axons.";
RL J. Cell Biol. 123:1463-1473(1993).
RN [4]
RP SEQUENCE OF 463-495 FROM N.A.
RX MEDLINE=92009921; PubMed=1833308;
RA Tse W.T., Menniger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
RA Lux S.E., Ward D.C., Forget B.G.;
RT "Isolation and chromosomal localization of a novel nonerythroid
RT ankyrin gene.";
RL Genomics 10:858-866(1991).
CC -1- FUNCTION: Attach integral membrane proteins to cytoskeletal
CC elements. Also bind to cytoskeletal proteins.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1 (SHOWN HERE), 2 AND 3; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
CC CELLS THROUGHOUT THE BRAIN.
CC -1- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
CC AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
CC AND FUNCTION (POTENTIAL).
CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
DR EMBL: X56957; CAA40278.1; -
DR EMBL: X56958; CAA40279.2; -
DR EMBL: Z28634; CABA2644.1; -
DR EMBL: M37123; AAA62828.1; -

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DR PIR: S14533; S14533.  
 DR PIR: R39643; A39643.  
 DR PIR: B39643; B39643.  
 DR PIR: S14569; S14569.  
 DR HSP: 000421; IAWC.  
 DR MIM: 106410; -.  
 DR InterPro: IPR002110; ANK.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR000906; ZU5.  
 DR Pfam: PF00023; ank; 24.  
 DR Pfam: PF00531; death; 1.  
 DR Pfam: PF00791; ZU5; 1.  
 DR PRINTS: PRO1415; ANKYRIN.  
 DR SMART: SM00248; ANK; 21.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00218; ZU5; 1.  
 DR PROSITE: PS50088; ANK\_REPEAT; 20.  
 DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 DR Cytochrome: Alternative splicing; Repeat; ANK repeat;  
 DR Phosphorylation.  
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 FT REPEAT 96 125 ANK 2.  
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 FT REPEAT 162 191 ANK 4.  
 FT REPEAT 193 220 ANK 5.  
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 FT REPEAT 16217 16246 REPEAT A.  
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 FT REPEAT 16313 16342 REPEAT A.  
 FT REPEAT 16345 16374 REPEAT A.  
 FT REPEAT 16377 16406 REPEAT A.  
 FT REPEAT 16409 16438 REPEAT A.  
 FT REPEAT 16441 16470 REPEAT A.  
 FT REPEAT 16473 16502 REPEAT A.  
 FT REPEAT 16505 16534 REPEAT A.  
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 FT REPEAT 16569 16598 REPEAT A.  
 FT REPEAT 16601 16630 REPEAT A.  
 FT REPEAT 16633 16662 REPEAT A.  
 FT REPEAT 16665 16694 REPEAT A.  
 FT REPEAT 16697 16726 REPEAT A.  
 FT REPEAT 16729 16758 REPEAT A.  
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 FT REPEAT 17209 17238 REPEAT A.  
 FT REPEAT 17241 17270 REPEAT A.  
 FT REPEAT 17273 17302 REPEAT A.  
 FT REPEAT 17305 17334 REPEAT A.  
 FT REPEAT 17337 17366 REPEAT A.  
 FT REPEAT 17369 1739

DR	PROSITE, PS50017; DEATH DOMAIN: 1
KM	Cytoskeleton; Repeat; ANK repeat; Phosphorylation; Lipoprotein
FT	DOMAIN 1 827
FT	DOMAIN 828 1386
FT	DOMAIN 1387 1862
FT	REPEAT 40 69
FT	REPEAT 73 102
FT	REPEAT 106 135
FT	REPEAT 139 168
FT	REPEAT 170 197
FT	REPEAT 201 230
FT	REPEAT 234 263
FT	REPEAT 267 296
FT	REPEAT 300 329
FT	REPEAT 333 362
FT	REPEAT 366 395
FT	REPEAT 399 428
FT	REPEAT 432 461
FT	REPEAT 465 494
FT	REPEAT 498 527
FT	REPEAT 531 560
FT	REPEAT 564 593
FT	REPEAT 597 626
FT	REPEAT 630 659
FT	REPEAT 663 692
FT	REPEAT 696 725
FT	REPEAT 729 758
FT	REPEAT 762 791
FT	DOMAIN 1399 1483
FT	SEQUENCE 1862 AA; 204242 MW; AE685B5B29001E5 CRC64;
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Query Match	18.1%; Score 137.5; DB 1; Length 1862;
Best Local Similarity	34.7%; Pred. No. 2.9e-05;
Matches 51; Conservative 17; Mismatches 68; Indels 11; Gaps	
OY	8 LATAARGVEEVRALLLEVALPNPNNSYGRPIOV-MMMSGARVAEILLLEGAPENCAD 66
DB	503 LATTARREGHVDPLALLDLKEASQACMTKGGTFLPHVAAKYGVKRLAELLLEHDARHPNAG 562
OY	67 PATLTRPVHDAAREGFDTL-VLHRAGARLDVRDAW-GRLPVDLAEELGHRDVARYL-- 122
DB	563 KNGLT-PLHVAVHNHNDLIVKLLPRGGS--PHSPAMNGYTPLHITAAKONQLEVARSLD 619
	123 ---RAAGGTRGSNHARIDAAEGSPDI 146
DB	620 YGGSANAESVGVTPLHLAAGEGHEM 646
RESULT 13	
YB23_HUMAN	STANDARD; PRT; 768 AA.
AC	Q9ULJ7; 16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Hypothetical protein KIAA1223 (Fragment).
GN	KIAA1223.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX	NCBI_Taxid=9606;
RN	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RX	MEDLINE=20039619; PubMed=10574462;
RA	Nagase T., Ishikawa K.-I., Kikuno R., Hirosewa M., Nomura N.,
RT	Ohara O.;
RA	"Prediction of the coding sequences of unidentified human genes. XV.

```

RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 6:337-345(1999).
CC -1- SIMILARITY: CONTAINS AT LEAST 14 ANK REPEATS.
CC
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CC -----
DR EMBL; AB033049; BAA86537.1; -.
DR HSSP; P42771; 1B17.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 13.
DR SMART; SM00248; ANK_13.
DR PROSITE; PS50086; ANK_REPEAT; 13.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW Hypothetical protein; Repeat; ANK repeat.
FT NON_TER
FT 1
FT REPEAT 1 1 ANK 1.
FT REPEAT 15 44 ANK 2.
FT REPEAT 48 82 ANK 3.
FT REPEAT 86 115 ANK 4.
FT REPEAT 119 148 ANK 5.
FT REPEAT 152 181 ANK 6.
FT REPEAT 185 214 ANK 7.
FT REPEAT 218 247 ANK 8.
FT REPEAT 251 280 ANK 9.
FT REPEAT 284 313 ANK 10.
FT REPEAT 317 346 ANK 11.
FT REPEAT 350 379 ANK 12.
FT REPEAT 383 412 ANK 13.
FT REPEAT 416 446 ANK 14.
SQ SEQUENCE 768 AA; 82819 MW; 2913B69BE2DE06D CAC64;

Query Match 17.6%; Score 133.5; DB 1; Length 768;
Best Local Similarity 33.8%; Pred. No. 2.6e-05;
Matches 49; Conservative 14; Mismatches 75; Indels 7; Gaps 3;

QY 8 LATAAARGVEEYRALLEVALPNAENSGRPIQY-NMGSARVAELLHGAEPCAD 66
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 124 LLAASMGHASYVNTLLFWGAVDSDISGRTVLSIASAQGVVEVRYTLDRGDENHRD 183
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 67 PATLLRPVDAAREGFLDTLVVLRAGACLDVDRDAGRLPVDAELGHRDVARYL--- 122
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 184 DAGWT-PLHMAFPEGRHLCEALIDEGATNTIDNDGRIFLLASQEGHYDCVQLLENK 242
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 123 -RAAAGTRGSNHARIDAEGPSDI 146
   |::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 243 SNIDRGYDGRNALRYVAALGHRDI 267
   |::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 14
ANK1_HUMAN STANDARD; PRT; 1880 AA.
AC P16157;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Ankyrin 1 (Erythrocyte ankyrin) (Ankyrin R).
GN ANK1 OR ANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.
RC TISSUE=Hematopoietic;
RX MEDLINE=90158830; PubMed=2137557;

```

RA Lux S.E., John K.M., Bennett V.;  
 RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated  
 RT structure with homology to tissue-differentiation and cell-cycle  
 RT control proteins.";  
 RL Nature 344:36-42(1990).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-90175370; PubMed-1689849;  
 RA Lambert S., Yu H., Pichal J.T., Lawler J., Ruff P., Speicher D.,  
 RA Cheung M.C., Kan Y.W., Palek J.;  
 RT "cDNA sequence for human erythrocyte ankyrin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).  
 [3]  
 RP VARIANT HS ILE-462.  
 RX MEDLINE-96225450; PubMed-8640229;  
 RA Eder S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,  
 RA Dornwell M., Heiders J., Kugler W., Oezcan R., Pekrun A.,  
 RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;  
 RT "Ankyrin-1 mutations are a major cause of dominant and recessive  
 RT hereditary spherocytosis.";  
 RL Nat. Genet. 13:214-218(1996).  
 CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL  
 CC ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO  
 CC NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE  
 CC CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.  
 CC ERYTHROCYTE ANKIRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE  
 CC CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;  
 CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC  
 CC PLASMA MEMBRANE.  
 CC -1- ALTERNATIVE PRODUCTS: At least 3 isoforms: 1/2.1 (shown here),  
 CC 2/2.2 and 3: are produced by alternative splicing.  
 CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).  
 CC -1- DISEASE: Defects in ANK1 are the cause of dominant and recessive  
 CC hereditary spherocytosis (HS).  
 CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.  
 CC -----  
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 CC -----  
 CC EMBL, X16609; CAA34610.1; -;  
 DE EMBL, M28880; AAA51732.1; -;  
 DE EMBL, S088275; SJHUK.  
 DR PIR, A35049; A35049.  
 DR HSP, G00421; IANC.  
 DR MIM, 182900; -;  
 DR InterPro: IPR002110; ANK.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR000906; ZUS.  
 DR Pfam, PF00023; ank; 23.  
 DR Pfam, PF00531; death; 1.  
 DR Pfam, PF00791; ZUS; 1.  
 DR PRINTS: PR01415; ANKYRIN.  
 DR SMART, SM00248; ANK; 22.  
 DR SMART, SM00005; DEATH; 1.  
 DR SMART, SM00218; ZUS; 1.  
 DR PROSITE, PS50088; ANK\_REPEAT; 20.  
 DR PROSITE, PS50097; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE, PS50017; DEATH\_DOMAIN; 1.  
 KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;  
 KW Phosphorylation; Lipoprotein; Disease mutation; Elliptocytosis;  
 KW Polymorphism.  
 FT INIT\_MET 0  
 FT DOMAIN 1 826 89 KDA DOMAIN (ANION EXCHANGE PROTEIN  
 FT BINDING DOMAIN).  
 FT DOMAIN 827 1381 62 KDA DOMAIN (SPECTRIN BINDING

FT	DOMAIN	1382	1880	DOMAIN
FT	REPEAT	43	72	55 KDA REGULATORY DOMAIN (REGULATES
FT	REPEAT	76	105	THE BINDING OF ANKYRIN TO SPECTRIN
FT	REPEAT	109	138	AND THE BAND 3 PROTEIN).
FT	REPEAT	142	171	ANK 1.
FT	REPEAT	173	200	ANK 2.
FT	REPEAT	204	233	ANK 3.
FT	REPEAT	237	266	ANK 4.
FT	REPEAT	270	299	ANK 5.
FT	REPEAT	303	332	ANK 6.
FT	REPEAT	336	365	ANK 7.
FT	REPEAT	369	398	ANK 8.
FT	REPEAT	402	431	ANK 9.
FT	REPEAT	435	464	ANK 10.
FT	REPEAT	468	497	ANK 11.
FT	REPEAT	501	530	ANK 12.
FT	REPEAT	534	563	ANK 13.
FT	REPEAT	567	596	ANK 14.
FT	REPEAT	600	629	ANK 15.
FT	REPEAT	633	662	ANK 16.
FT	REPEAT	666	695	ANK 17.
FT	REPEAT	699	728	ANK 18.
FT	REPEAT	732	761	ANK 19.
FT	REPEAT	765	794	ANK 20.
FT	DOMAIN	1402	1486	ANK 21.
FT	VARSPLIC	1512	1873	ANK 22.
FT	VARSPLIC	1874	1874	ANK 23.
FT	VARSPLIC	1849	1880	MISSING (IN ISOFORM 2).
FT	VARIANT	20	20	H -> D (IN ISOFORM 2).
FT	VARIANT	462	462	TVEGLEPSELEVDIDYEMKSHKDHSTPNP -> ELRGS
FT	VARIANT	618	618	GLQPDLEGRKGAQYKRASLKRKGQ (IN ISOFORM
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FT	VARIANT	844	844	R -> T.
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FT	VARIANT	1545	1545	/FTID=VAR_000738.
FT	VARIANT	1545	1545	/FTID=VAR_000739.

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RESULT 15
DAPK_HUMAN STANDARD; PRT; 1431 AA.
ID DAPK_HUMAN
AC P53355;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Death-associated protein kinase 1 (EC 2.7.1.-) (DAP kinase 1).
GN DAPK1 OR DAPK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95129831; Pubmed=7828849;
RA Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;
RT "Identification of a novel serine/threonine kinase and a novel 15-KD
RT protein as potential mediators of the gamma interferon-induced cell
RT death.";
PM Genes Dev. 9:15-30(1995).
[2]
RP REVISIONS TO 164-171.
RA Feinstein E.;
RU Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL
CC DEATH.
CC -!- PTM: AUTOPHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 10 ANK REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X76104; CAA53712.1; -.
CC DR HSSP: 063450; 1A06.
CC DR MIM: 600831; -.
CC DR InterPro: IPR002110; ANK.
CC DR InterPro: IPR000488; Death.
CC DR InterPro: IPR000719; Euk_pkinase.
CC DR InterPro: IPR002290; Ser_thr_pkinase.
CC DR Pfam: PF00023; ank. 8.
CC DR Pfam: PF00531; death. 1.
CC DR Pfam: PF00069; pkinase. 1.
CC DR SMART: SM00248; ANK; 7.
CC DR SMART: SM00005; DEATH; 1.
CC DR SMART: SM00220; S_TKC; 1.
CC DR PROSITE: PS50088; ANK_REPEAT; 6.
CC DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
CC DR PROSITE: PS50017; DEATH_DOMAIN; 1.
CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
CC DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC DR Transferase: Serine/threonine-protein kinase; Calmodulin-binding;
CC KM Phosphorylation: ATP-binding; Repeat: ANK repeat; Apoptosis.
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## OM protein - protein search, using sw model

Run on: September 19, 2002, 17:24:02 : Search time 26.94 Seconds

(without alignments)  
950.380 Million cell updates/sec

Title: US-09-016-869b-35

Perfect score: 760  
Sequence: 1 MEPSADWLATAAARGRYEV.....TRGSNHARIDAEGPSDIPD 148

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	72.1	106	4 Q9NP05	Q9np05 homo sapien
2	512	67.4	130	11 Q91YF9	Q91yF9 mesocricetu
3	510	67.1	157	11 Q9B033	Q9B033 mesocricetu
4	501	65.9	144	11 Q99PH0	Q99pH0 mesocricetu
5	476.5	62.7	152	11 Q9R023	Q9r023 rattus norv
6	476	62.6	168	11 P97510	P97510 mus musculu
7	474	62.4	168	11 Q89088	Q89088 mus musculu
8	449	59.1	102	6 Q9X551	Q9x551 felis silve
9	444	58.4	103	6 Q9T5Y1	Q9t5Y1 sus scrofa
10	427	56.2	86	6 Q9X552	Q9x552 felis silve
11	409	53.8	81	6 Q9GMF2	Q9gmF2 canis fami
12	408	53.7	86	11 Q900P0	Q9q0P0 mus musculu
13	408	53.7	86	11 Q921C1	Q921C1 mus musculu
14	407	53.6	86	6 Q9T5Y0	Q9t5Y0 sus scrofa
15	405	53.3	86	11 Q54846	Q54846 mus musculu
16	334	43.9	113	11 Q921C2	Q921C2 mus musculu

17	331	43.6	113	11 Q9QWH5	Q9qwh5 mus musculu
18	327	43.0	113	11 Q9QWH8	Q9qwh8 mus musculu
19	326	42.9	113	11 Q9QWH7	Q9qwh7 mus musculu
20	326	42.9	113	11 Q9QWH6	Q9qwh6 mus musculu
21	314.5	41.4	112	11 Q9QWH4	Q9qwh4 mus musculu
22	292	38.4	124	13 P70067	P70067 xiphophorus
23	290	38.2	124	13 Q9W618	Q9w618 xiphophorus
24	282	37.1	124	13 Q9DE56	Q9de56 fugu rubrip
25	264.5	34.8	164	13 Q9DE53	Q9de53 fugu rubrip
26	254	33.4	166	11 Q91YV3	Q91yV3 mus musculu
27	234	30.8	58	6 Q97886	Q97886 equus cabal
28	231.5	30.5	168	11 Q9D153	Q9d153 mus musculu
29	209	27.5	116	4 Q95440	Q95440 homo sapien
30	157	20.7	843	11 P97582	P97582 rattus norv
31	149.5	19.7	1101	4 Q9NXY9	Q9nxy9 homo sapien
32	146	19.2	1166	4 Q9H2K2	Q9h2K2 homo sapien
33	146	19.2	1265	4 Q9HAS4	Q9has4 homo sapien
34	142	18.7	42	11 Q9Z1E8	Q9z1E8 mus musculu
35	138	18.2	1136	6 Q9N180	Q9n180 bos taurus
36	137.5	18.1	1098	11 Q61304	Q61304 mus musculu
37	137.5	18.1	1848	11 Q61302	Q61302 mus musculu
38	137	18.0	299	11 Q91WK7	Q91wk7 mus musculu
39	137	18.0	300	4 Q9UGV1	Q9ugv1 homo sapien
40	137	18.0	40	4 Q95271	Q95271 homo sapien
41	136	17.9	1327	4 Q921C3	Q921C3 mus musculu
42	134.5	17.7	782	4 Q9BZ14	Q9bz14 homo sapien
43	134.5	17.7	968	5 Q9VCM6	Q9vcm6 drosophila
44	134	17.6	1181	5 Q9X237	Q9x237 drosophila
45	134	17.6	1181	5 Q9VBP3	Q9vbp3 drosophila

## ALIGNMENTS

RESULT	ID	Q9NP05	PRELIMINARY:	PRT:	106 AA.
Q9NP05	Q9NP05	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	CDK41 PROTEIN (FRAGMENT).				
GN	CDK41.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euthera; Primates; Carnivora; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=94203288; PubMed=8152487;				
RA	Nobori T., Miura K., Wu D.J., Lois A., Takabayashi K., Carson D.A.;				
RT	"Deletions of the cyclin-dependent kinase-4 inhibitor gene in multiple human cancers."				
RT	Nature 368:753-756(1994).				
DR	EMBL: S69824; AADI4050.1; .				
DR	EMBL: S69822; AADI4050.1; JOINED.				
DR	HSP: P42771; 1B17.				
DR	InterPro: IPR002110; ANK.				
DR	PROSITE: PS50297; ANK_REPEAT_REGION; 1.				
KW	ANK repeat; Repeat.				
FT	NON_TER				
SO	SEQUENCE				

Query Match 72.1%; Score 548; DB 4; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.3e-39; Indels 0; Gaps 0;  
Matches 106; Conservative 0; Mismatches 0;

QY	43 VMWGSARVAEILLGAPNCADPATLTPYDARREGFLTLVLRHAGARLDVRAW 102
DB	1 VMWGSARVAEILLGAPNCADPATLTPYDARREGFLTLVLRHAGARLDVRAW 60
QY	103 GRPVDLAETIGHRDVARYLRAAAGTRGSNHARIDAEGPSDIPD 148

Db 61 GRPVDLAELGHRVARYLRAAGGTGCSNHARIDAEGSPDIPD 106

## RESULT 2

Q91PF9 PRELIMINARY: PRT: 130 AA.  
 AC Q91PF9;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE P15INK4B CYCLIN-DEPENDENT KINASE INHIBITOR.  
 GN P15INK4B.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 NC NCBL\_TaxId=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE-PANCREAS;  
 RA Muscarella P., Ulrich A.B., Casto B.C., Montaux N., Knobloch T.J.,  
 Witel U.A., Melvin S., Pour P.M., Song H., Gold B., Batra S.K.,  
 Weghorst C.M.;  
 RT "Homozygous Deletion of P15INK4B/P16INKA Gene Locus in Syrian Golden  
 RT Hamster Tumor Cell Lines."  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ302037; CNC67498.1; -  
 KW Kinase; Cyclin.  
 SQ SEQUENCE 130 AA; 13842 MW; 4C04DD3F8C6FEF013 CRC64;

Query Match 67.4%; Score 512; DB 11; Length 130;  
 Best Local Similarity 85.0%; Pred. No. 3.3e-36;  
 Matches 102; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 8 LATPAARGVEEYRALLEVALPNAPNSTGRPIQVMMGSAKYAEELLHGAEPNCADP 67  
 Db 10 LATPAARGVEYRQLLEAGVDPNANRPRPIQVMMGSTQVALLLELHGAEPNCADP 69  
 QY 68 ATTTPRVHDAAREGFDTLVVLRAGARLDVDRDAGRLPVDLAELGHRVARYLRAAG 127  
 Db 70 NTLTRPVHDAAREGFDTLVVLRAGARLDVDRDAGRLPVDLAELGHRVARYLRAAG 129

RESULT 3  
 Q9EO33 PRELIMINARY: PRT: 157 AA.  
 Q9EO33;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR 2.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 NC NCBL\_TaxId=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Muscarella P., Knobloch T.J., Weghorst C.M.;  
 RT "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and  
 RT Identification of Inactivating Alterations in Hamster Tumor Cell  
 RT Lines."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF292567; AAG44950.1; -  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR SMART: SM00248; ANK; 4.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.  
 SQ SEQUENCE 157 AA; 16635 MW; 06FD66AEB6B30DCFB CRC64;

Query Match 67.1%; Score 510; DB 11; Length 157;  
 Best Local Similarity 68.9%; Pred. No. 6e-36;  
 Matches 102; Conservative 17; Mismatches 29; Indels 0; Gaps 0;

QY 1 MEPSADWLATAARGVEEYRALLEVALPNAPNSTGRPIQVMMGSAKYAEELLHGA 60  
 Db 1 MEPSADGLARAAAGREDEVRALLEAGVSPNAPNCFGRTPIOVMMGNTQVARRLLLYGA 60  
 QY 61 EPNCAADPATLTPRVHDAAREGFDTLVVLRAGARLDVDRDAGRLPVDLAELGHRVARY 120  
 Db 61 EPNCEADPATLSRPVHDAAREGFDTLVVLRAGARLDVDRDAGRLPVDLAELGHRVARY 120  
 QY 121 YLRAAGTGRGSHARIDAEGSPDIPD 148  
 Db 121 YLRAAGNTPQSGSEPGVTSQTPPEVSD 148

## RESULT 4

Q99PHO PRELIMINARY: PRT: 144 AA.  
 AC Q99PHO;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE CYCLIN-DEPENDENT CELL CYCLE INHIBITOR (FRAGMENT).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 NC NCBL\_TaxId=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Muscarella P., Knobloch T.J., Weghorst C.M.;  
 RT "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and  
 RT Identification of Inactivating Alterations in Hamster Tumor Cell  
 RT Lines."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF291998; AAG59801.1; -  
 DR EMBL: AF291997; AAG59801.1; JOINED.  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR SMART: SM00248; ANK; 4.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Repeat.  
 FT NON\_TER 144  
 SQ SEQUENCE 144 AA; 15206 MW; 8904FP9C0C316A084 CRC64;

Query Match 65.9%; Score 501; DB 11; Length 144;  
 Best Local Similarity 70.6%; Pred. No. 3.2e-35;  
 Matches 101; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 MEPSADWLATAARGVEEYRALLEVALPNAPNSTGRPIQVMMGSAKYAEELLHGA 60  
 Db 1 MEPSADGLARAAAGREDEVRALLEAGVSPNAPNCFGRTPIOVMMGNTQVARRLLLYGA 60  
 QY 61 EPNCAADPATLTPRVHDAAREGFDTLVVLRAGARLDVDRDAGRLPVDLAELGHRVARY 120  
 Db 61 EPNCEADPATLSRPVHDAAREGFDTLVVLRAGARLDVDRDAGRLPVDLAELGHRVARY 120  
 QY 121 YLRAAGTGRGSHARIDAEGSPDIPD 143  
 Db 121 YLRAAGNTPQSGSEPGVTSQTP 143

## RESULT 5

Q9R023 PRELIMINARY: PRT: 159 AA.  
 AC Q9R023;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)



DE P16 PROTEIN p16INK4A.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=F344/N; TISSUE=LUNG;  
RX MEDLINE=97184461; PubMed=9032263;  
RA Swatford D.S., Middleton S.K., Palmisano W.A., Nikula K.J.,  
RA Testaijezi J., Baylin S.B., Herman J.G., Belinsky S.A.;  
RT "Frequent aberrant methylation of p16INK4a in primary rat lung  
tumors";  
RL Cell. Biol. 17:1366-1374(1997).  
DR EMBL; L81167; AAD48924.1; -.  
DR HSSP; P42771; 1B17.  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 4.  
DR SMART; SM00248; ANK; 1.  
DR PROSITE; PS50297; ANK\_REP\_REGION; 1.  
DR ANK repeat; Repeat.  
SS SEQUENCE 159 AA; 17366 MW; 3C4CA920A1FEAEB6 CRC64;

Query Match	62.7%	Score 476.5;	DB 11;	Length 159;
Best local Similarity	74.6%;	Pred. No. 4.2e-33;		
Matches	97; Conservative	11; Mismatches	19; Indels	3; Gaps
OY	1	MEPSADMLATAARCRVEEVRALLAEVALP.NPNPSNGRRPIOVMMGSA.RVAVELLLHGA	60	
				: :       :
Db	1	MSSSDRLARAALGREHYRALLERGSAPNPNTFGRRPIOVMMGNKVALLLSYGA	60	
OY	61	EENCADPATLTFRPVHDAAAREGF.LDTLVYLHRAGARLDVDAMGR.LP.VDLAEELGHQDVNR	120	
	:	:	:	:
Db	61	DSCNCEPTTLSPRVHDAAAREGF.LD.TLVYLHQGARLR.DVDAMGR.LP.DLALRGHHQDVNR	120	
OY	121	YLR---AANG	127	
		: :		
Db	121	YLR.YLLSAG	130	

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RESULT      6
P97510
ID      P97510      PRELIMINARY;      PRT;      168 AA.
AC      P97510. P97937;
DT      01-MAY-1997 (TReMBLrel. 03, Created)
DT      01-MAY-1999 (TReMBLrel. 10, last sequence update)
DT      01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE      CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR
DE      PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR 2A) (P16INK4A) (CYCLIN-
DE      DEPENDENT KINASE INHIBITOR PROTEIN).
GN      CDKN2A OR E1A1PHA OR P16INK4A.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_taxid=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-DBA/2N; TISSUE-SPLEEN.
RX      MEDLINE=98151529; PubMed=9482902;
RA      Zhang S., Ramsay E.S., Wock B.A.;
RT      "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and
RT      p16ARF, is a candidate for the plasmacytoma susceptibility locus,
RT      pCt1."
RL      Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
RN      [2]
RP      SEQUENCE OF 1-42 FROM N.A.
RC      STRAIN-VARIOUS STRAINS.
RX      MEDLINE=97179476; PubMed=9021155;
RA      Hertzog C.R., You M.;
RT      "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
RT      suppressor gene."
RL      Mamm. Genome 8:65-66(1997).

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RN [13]  
 RP SEQUENCE OF 1-155 FROM N.A.  
 RC STRAIN=C57BL/6J X DBA;  
 RA Matumbres M., Melendez B., Mangués R.,  
 RN Serrano M., Pellicer A., Fernandez-Piqueras J.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [14]  
 RP SEQUENCE OF 1-42 FROM N.A.  
 RC STRAIN=DBA/2, AND C57BL/6;  
 RX MEDLINE=95380169; PubMed=7651726;  
 RA Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,  
 RN Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;  
 RL "Cloning and characterization of murine p16INK4a and p15INK4b genes.";  
 RX Oncogene 11:635-645(1995).  
 RN [15]  
 RP SEQUENCE OF 1-42 FROM N.A.  
 RC STRAIN=DBA/2, AND C57BL/6;  
 RX Gressani K.M., Rollins L.A., Miller M.S.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE OF 1-11 FROM N.A.  
 RC STRAIN=ICR SWISS;  
 RX Medline=97128829; PubMed=8973369;  
 RA Soloff E.V., Herzog C.R., You M.;  
 RT "The 5'-flanking region of the E1 alpha form of the murine p16INK4a  
 RT Gene 180:213-215(1996).  
 RL [17]  
 RP SEQUENCE OF 1-42 FROM N.A.  
 RC STRAIN=CAST/Ei, C57BL/6J, ARF/J, AND MOLE/Ei;  
 RA Santos J., Melendez B., Perez de Castro I., Matumbres M., Serrano M.,  
 RN Pellicer A., Fernandez-Piqueras J.;  
 RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
 RT in mouse inbred strains.";  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ;  
 RA Gong Z., Li J., Fu J.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF044336; AAC08963.1; -  
 DR EMBL: U49280; AAC00052.1; -  
 DR EMBL: U66087; AAB39600.1; -  
 DR EMBL: U66086; AAB39600.1; JOINED.  
 DR EMBL: AF004588; AAB61416.1; -  
 DR EMBL: U47018; AAC52987.1; -  
 DR EMBL: U79628; AAD00226.1; -  
 DR EMBL: U79625; AAD00223.1; -  
 DR EMBL: U79627; AAD00225.1; -  
 DR EMBL: AF321190; AAK83159.1; -  
 DR HSSP: P42771; 1B17.  
 DR MGD: MGI:104738; Cdkn2a.  
 DR Interpro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 4.  
 DR SMART: SM00248; ANK; 1.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 DR ANK repeat; Cyclin; Kinase; Repeat.  
 KW ANK repeat; Cyclin; Kinase; Repeat.  
 SQ SEQUENCE 168 AA; 17941 MW; 9A6B0F24F34D5FEC CRC64;

[illegible]

OY 121 YLRAA-----AGCT--RGSNHARIDAEGPSDIP 147  
 DB 121 YLRSAGCSLCSAGWSLCTAGNVAQTGDGHSFSSSTP 155

RESULT 7  
 ID 089088 PRELIMINARY; PRT; 168 AA.

AC 089086;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CYCLIN DEPENDENT KINASE INHIBITOR p16INK4A (p16INK4A TUMOR SUPPRESSOR PROTEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).  
 GN CDKN2A OR E1ALPHA OR P16.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]

SEQUENCE FROM N.A.  
 STRAIN=BALB/CANP; TISSUE=SPLEEN;  
 MEDLINE=98151529; PubMed=9482902;  
 RA Zhang S., Ramsay E.S., Mock B.A.;  
 RT "cdk2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and p19ARF, is a candidate for the plasmacytoma susceptibility locus,  
 RT Pctrl.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).  
 RN [2]

RP SEQUENCE OF 1-42 FROM N.A.

RC STRAIN=MA/MAJ;  
 RX MEDLINE=97179476; PubMed=9021155;

RA Herzog C.R., You W.;  
 RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor suppressor gene";  
 RL Mamm. Genome 8:65-66(1997).  
 RN [3]

RP SEQUENCE OF 1-42 FROM N.A.  
 RC STRAIN=BALB/CJ AND MUS MUS POSCHIAVINUS;  
 RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M., Pelllicer A., Fernandez-Piqueras J.;  
 RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains";  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF044335; AAC008962.1; -;  
 DR EMBL: U99279; AAC00051.1; -;  
 DR EMBL: U79626; AAD00224.1; -;  
 DR HSSP: P42771; 1B17.  
 MCD: MGI:104738; Cdkn2a.  
 InterPro: IPR002110; ANK.

DR Pfam: PF000023; ank; 4.  
 DR SMART: SM00248; ANK; 1.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Cyclin; Kinase; Repeat.  
 SO SEQUENCE 168 AA; 17915 MW; 3564973BEAC4D167 CRC64;

Query Match 62.4%; Score 474; DB 11; Length 168;  
 Best Local Similarity 63.2%; Pred. No. 7.3e-33;  
 Matches 98; Conservative 17; Mismatches 32; Indels 8; Gaps 2;

OY 1 MESAAMWLATAARGRVEYRALLLEVALPAPNSTGRPIOVMMGSAARVAELLHGA 60  
 DB 1 MESAAMWLATAARGRVEYRALLLEVALPAPNSTGRPIOVMMGSAARVAELLHGA 60  
 OY 61 EPACADPATITRPVHDAREGFLDTLVVLRAGARLDVADAGRLPYDLAEELGRDVAR 120  
 DB 61 DSNCEPTPTFSRPVHDAREGFLDTLVVLRAGARLDVADAGRLPYDLAEELGRDVAR 120  
 OY 121 YLRAA-----AGGT--RGSNHARIDAEGPSDIP 147  
 DB 121 YLRSAGCSLCSAGWSLCTAGNVAQTGDGHSFSSSTP 155

RESULT 8  
 ID 09XS51 PRELIMINARY; PRT; 102 AA.

AC 09XS51;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE P16/CDKN2A/MTS1 (FRAGMENT).  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxId=9685;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=PERIPHERAL BLOOD;  
 RA Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y., Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.;  
 RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A) and p15(MTS2/CDKN2B).";  
 RL EMBL: AB010807; BAA33540.1; -;  
 DR HSSP: P42771; 1B17

DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 3.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Repeat.  
 FT NON\_TER 1  
 FT NON\_TER 102  
 SQ SEQUENCE 102 AA; 10824 MW; 26399FF21359F35D CRC64;

Query Match 59.1%; Score 449; DB 6; Length 102;  
 Best Local Similarity 86.0%; Pred. No. 5.5e-31;  
 Matches 86; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

OY 43 VMMSGARVAELLHLHGAEPNCADPATITRPVHDAREGFLDTLVVLRAGARLDVADAW 102  
 DB 1 VMMSGARVAELLHLHGAEPNCADPATITRPVHDAREGFLDTLVVLRAGARLDVADAW 60  
 OY 103 GRLPYDLAEELGRHVARVLRAGAGTGSNHARIDAEG 142  
 DB 61 GRLPYDLAEELGRHVARVLRAGAGTGSNHARIDAEG 100

RESULT 9  
 ID 09TSY1 PRELIMINARY; PRT; 103 AA.

AC 09TSY1;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR, P16 (FRAGMENT).  
 GN CDKN2A.

OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suis.  
 OX NCBI\_TaxId=9823;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=LARGE WHITE;  
 RA Le Chalony C., Hayes H., Frelat G., Geffroin C.;  
 RT "Identification and mapping of swine CDKN2A and CDKN2B exon2 sequences";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ242787; CAB65454.1; -;  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 2.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.  
 FT NON\_TER 1  
 FT NON\_TER 103

```
SQ SEQUENCE 103 AA: 11023 MW: 5D23ABCC108BDE0B CRC64:

Query Match
Best Local Similarity 84.3%; Score 444; DB 6; Length 103;
Matches 86; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 43 VMMGSAARVAELLHLHGAEPNCADPATLTTRPVDAAREGFLDTLVVLRHAGARLDVDRAM 102
D 1 VMMGSAARVAELLHLHGAEPNCADPATLTTRPVDAAREGFLDTLVVLRHAGARLDVDRAM 60
DB 103 GRLPVDLAEEIGHRDVARYLRAAAGSTRGSNHRIDAAGPS 144
61 GRLPVDLAEEIGHRDVARYLRAAAGSTRGSNHRIDAAGPS 102

RESULT 10
Q9XS52 PRELIMINARY; PRT; 86 AA.
Q9XS52:
01-NOV-1999 (TREMblrel. 12, Created)
01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE p15/MTS2/CDKN2B (FRAGMENT).
OS Felis silvestris catus (cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
RA Okada M., Cho K., Setoguchi A., Minehata K., Yawata M., Endo Y.,
RA Nishiyaki K., Watari T., Tsujimoto H., Hasegawa A.;
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
RT and p15(MTS2/CDKN2B).";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB010808; BAA3541.1; -
DR HSSP: P42771; 1B17
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 2.
DR PROSITE: PS50297; ANK_REGION; 1.
KW ANK repeat; Repeat.
FT NON_TER 1
SQ SEQUENCE 86 AA: 9340 MW: AS9F0193290E867 CRC64:

Query Match
Best Local Similarity 56.2%; Score 427; DB 6; Length 86;
Matches 83; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 43 VMMGSAARVAELLHLHGAEPNCADPATLTTRPVDAAREGFLDTLVVLRHAGARLDVDRAM 102
D 1 VMMGSAARVAELLHLHGAEPNCADPATLTTRPVDAAREGFLDTLVVLRHAGARLDVDRAM 60
DB 103 GRLPVDLAEEIGHRDVARYLRAAAG 127
61 GRLPVDLAEEIGHRDVARYLRAAAG 85

RESULT 11
Q9GMF2 PRELIMINARY; PRT; 81 AA.
Q9GMF2:
01-MAR-2001 (TREMblrel. 16, Created)
01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE p15/MTS2/CDKN2B (FRAGMENT).
OS Felis silvestris catus (cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.

RA Venkataraj V.S., Mayor J., Modiano J.F.;
RT "Role of p16/INK4a in familial canine cancers.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF234176; AAG01087.1; -
DR HSSP: P42771; 1B17.
DR InterPro: IPR002110; ANK.
DR PROSITE: PS50297; ANK_REGION; 1.
KW ANK repeat; Kinase; Repeat.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA: 8868 MW: 0E39D8D805BAC0F CRC64:

Query Match
Best Local Similarity 53.8%; Score 409; DB 6; Length 81;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 43 VMMGSAARVAELLHLHGAEPNCADPATLTTRPVDAAREGFLDTLVVLRHAGARLDVDRAM 102
D 1 VMMGSAARVAELLHLHGAEPNCADPATLTTRPVDAAREGFLDTLVVLRHAGARLDVDRAM 60
DB 103 GRLPVDLAEEIGHRDVARYL 122
61 GRLPVDLAEEIGHRDVARYL 80

RESULT 12
Q9QUP0 PRELIMINARY; PRT; 86 AA.
Q9QUP0:
01-MAY-2000 (TREMblrel. 13, Created)
01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE p15/MTS2/CDKN2B (FRAGMENT).
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
RA Pellicer A., Fernandez-Piqueras J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
RT in mouse inbred strains.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U79639; AAD00234.1; -
DR EMBL: U79636; AAD00232.1; -
DR EMBL: U79638; AAD00233.1; -
DR HSSP: P42771; 1B17.
DR InterPro: IPR002110; ANK.
DR PROSITE: PS50297; ANK_REGION; 1.
KW ANK repeat; Cyclin; Kinase; Repeat.
FT NON_TER 1
FT NON_TER 86
SQ SEQUENCE 86 AA: 9269 MW: 509DB3613251B18 CRC64:

Query Match
Best Local Similarity 53.7%; Score 408; DB 11; Length 86;
Matches 79; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 43 VMMGSAARVAELLHLHGAEPNCADPATLTTRPVDAAREGFLDTLVVLRHAGARLDVDRAM 102
D 1 VMMGSAARVAELLHLHGAEPNCADPATLTTRPVDAAREGFLDTLVVLRHAGARLDVDRAM 60
DB 103 GRLPVDLAEEIGHRDVARYLRAAAG 127
61 GRLPVDLAEEIGHRDVARYLRAAAG 85

RESULT 13
```

```
Q92IC1
ID Q92IC1 PRELIMINARY; PRT; 86 AA.
AC Q92IC1;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
GN P15(INK4B).
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
RA Pellicer A., Fernandez-Piqueras J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
RT in mouse inbred strains.";
RT Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
HSSP; P42771; 1B17.
EMBL; U79637; AAC00237.1; -.
DR InterPro: IPR002110; ANK.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Kinase; Repeat.
FT NON_TER 1
FT NON_TER 86
SQ SEQUENCE 86 AA; 9269 MW; 509D9B3613251B18 CRC64;

Query Match 53.7%; Score 407; DB 11; Length 86;
Best Local Similarity 92.9%; Pred. No. 1.4e-27;
Matches 79; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 43 VMMGSAVAVALLLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDDAW 102
DB 1 VMMGSAQVAVELLHLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDDAW 60
QY 103 GRLPVDLAELGHRDVARYLRAAG 127
DB 61 GRLPVDLAEBQGHRIARYLHAATG 85

RESULT 14
Q9TSYO PRELIMINARY; PRT; 86 AA.
AC Q9TSYO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).
GN CDKN2B.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LARGE WHITE;
RA MEDLINE=20290998; PubMed=10828598;
RA Le Chalony C., Hayes H., Fretat G., Geffrotin C.;
RT "Identification and mapping of swine cyclin-dependent kinase inhibitor
RT CDKN2A and CDKN2B exon2 sequences.";
RT Cytogenet. Cell Genet. 88:240-243(2000).
RL EMBL; AJ242788; CAB65455.1; -.
DR HSSP; P42771; 1B17.
DR InterPro: IPR002110; ANK.
DR Pfam; PF00023; ank; 2.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Kinase; Repeat.
FT NON_TER 1
FT NON_TER 86
SQ SEQUENCE 86 AA; 9286 MW; 16EF7A223293CFC9 CRC64;
```

```
Query Match 53.6%; Score 407; DB 6; Length 86;
Best Local Similarity 92.9%; Pred. No. 1.7e-27;
Matches 79; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 43 VMMGSAVAVALLLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDDAW 102
DB 1 VMMGSAQVAVELLHLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDDAW 60
QY 103 GRLPVDLAELGHRDVARYLRAAG 127
DB 61 GRLPVDLAEBQGHRIARYLHAASG 85

RESULT 15
Q54846 PRELIMINARY; PRT; 86 AA.
AC Q54846;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15INK4B (FRAGMENT).
GN CDKN2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA MEDLINE=99124385; PubMed=9927195;
RA Malumbres M., de Castro I.P., Santos J., Piqueras J.F., Pellicer A.;
RT "Hypemethylation of the cell cycle inhibitor p15INK4b 3'-untranslated
RT region interferes with its transcriptional regulation in primary
RT lymphomas.";
RT Lymphomas";
RL Oncogene 18:385-396(1999).
DR EMBL; AF015460; AAB94534.1; -.
DR HSSP; P42771; 1B17.
DR InterPro: IPR002110; ANK.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Kinase; Repeat.
FT NON_TER 1
FT NON_TER 9237
SQ SEQUENCE 86 AA; 9237 MW; 0499DB26144FB6DF CRC64;
```

```
Query Match 53.3%; Score 405; DB 11; Length 86;
Best Local Similarity 91.8%; Pred. No. 2.4e-27;
Matches 78; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 43 VMMGSAVAVALLLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDDAW 102
DB 1 VMMGSAQVAVELLHLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDDAW 60
QY 103 GRLPVDLAELGHRDVARYLRAAG 127
DB 61 GRLPVDLAEBQGHRIARYLHAASG 85
```

Search completed: September 19, 2002, 17:27:56  
Job time: 234 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:23:01 : Search time 30.1 Seconds

(without alignments)  
546.144 Million cell updates/sec

Title: US-09-016-869B-35

Perfect score: 760  
Sequence: 1 MESPADWLATAARGRVEEV.....TRGSNHRARIDAEGSPDIPD 148

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	760	100.0	148	AA81701	Multiple tumour su
2	760	100.0	148	AA80940	Human multiple tum
3	760	100.0	151	AA853401	Inhibitor of cyclin
4	760	100.0	156	AA85116	Cell-cycle regulat
5	760	100.0	156	AA24741	Human INK-4 protei
6	760	100.0	156	AA188354	Human cell cycle r
7	760	100.0	391	AAW23534	CDK Inhibitory f
8	760	100.0	391	AAW95094	Human p27-p16 fus
9	760	100.0	391	AA197526	Human W3 protein s
10	760	100.0	391	AA196041	Antiproliferative
11	760	100.0	391	AA196068	Angiogenesis inh

12	753	99.1	156	AA10627	Tumour suppressor
13	753	99.1	156	AA19251	Human multiple tum
14	753	99.1	156	AAW74549	Amino acid sequenc
15	753	99.1	156	AAW40524	Human MTS1 protein
16	753	99.1	156	AAW80524	A human multiple t
17	753	99.1	156	AA15448	Human MTS1 protein
18	753	99.1	156	AA197524	Human p16 protein
19	753	99.1	156	AA197524	Human cyclin depen
20	753	99.1	156	AA196053	Human cyclin depen
21	753	99.1	156	AA196067	Human multiple tum
22	753	99.1	156	AA192921	Human multiple tum
23	753	99.1	156	AA191102	Human MTS1 protein
24	753	99.1	156	AA159415	Human multiple tum
25	753	99.1	156	AA154902	Human multiple tum
26	753	99.1	156	AAU02122	Human multiple tum
27	753	99.1	156	AAE01002	Protein encoded by
28	753	99.1	156	AA197334	Human Multiple Tum
29	753	99.1	156	AA196890	Human W9 protein s
30	753	99.1	228	AA197522	Antiproliferative
31	753	99.1	228	AA196051	Angiogenesis inh
32	753	99.1	228	AA196078	Truncated p27/p16
33	753	99.1	237	AAW95105	Human W9 protein s
34	753	99.1	237	AA197534	Antiproliferative
35	753	99.1	237	AA196049	Angiogenesis inh
36	753	99.1	252	AA196076	Truncated p27/p16
37	753	99.1	252	AA197535	Human M10 protein
38	753	99.1	252	AA196050	Antiproliferative
39	753	99.1	252	AA196077	Angiogenesis inh
40	753	99.1	323	AA196079	Secretable angio
41	753	99.1	323	AA196079	Truncated p27/p16
42	753	99.1	334	AAW95103	Human W8 protein s
43	753	99.1	334	AA197532	Antiproliferative
44	753	99.1	334	AA196074	Angiogenesis inh
45	753	99.1	365	AAW23536	CDK inhibitory fus

#### ALIGNMENTS

RESULT 1	
AA81701	
ID	AA81701 standard; Protein; 148 AA.
XX	
AC	AA81701;
XX	
DT	08-MAY-1996 (first entry)
DE	Multiple tumour suppressor 1 (MTS1) polypeptide.
XX	
KW	Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
KW	predisposition; melanoma; leukaemia; lymphoma; prognosis;
KW	pancreas; breast; thyroid.
XX	
OS	Homo sapiens.
XX	
PN	W09525813-A1.
XX	
PD	28-SEP-1995.
XX	
PF	17-MAR-1995; 95WO-US03537.
XX	
PR	01-JUN-1994; 94US-0251938.
PR	18-MAR-1994; 94US-0214582.
PR	18-MAR-1994; 94US-0215086.
PR	18-MAR-1994; 94US-0215087.
XX	
XX	14-APR-1994; 94US-0227369.
PA	(MYRI-) MYRIAD GENETICS INC.
XX	(UTAH) UNIV UTAH RES FOUND.
XX	
PI	Cannon-Albright LA, Kamb A, Skolnick MH;
XX	
DR	WPI; 1995-344626/44.

DR N-PSDB: AAT00736.  
 XX Detecting polymorphism associated with cancer pre-disposition - also  
 PT DNA, vectors and host cells e.g. for gene or protein replacement  
 PT therapy and drug screening  
 XX  
 PS Example 8; Pages 92-93; 148pp; English.  
 XX  
 CC An individual can be diagnosed as having a predisposition to cancer  
 CC by detecting an alteration in the wild type multiple tumour  
 CC suppressor (MTS) gene, using gene probes which hybridise to the MTS1  
 CC gene ORF AAT00736 (which encodes AAR81701) mutant sequences AAT00749/50.  
 CC The above assay can also be used in the diagnosis and prognosis of  
 CC melanoma, lymphoma, leukaemia and pancreas, breast and thyroid  
 CC cancers, etc..  
 CC  
 XX Sequence 148 AA:  
 SQ

Query Match 100.0%; Score 760; DB 16; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 6,6e-83;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEPSADWLATAARGVEEVRALLEAVALPNAPNSYGRPRIOYMMGASARVAELLHGA 60  
 Db 1 mepsadwlataaargveevrallleavalpnapsygrpridyvmngsarvaeilllhga 60  
 OY 61 EPNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVDMGRLPVDLAEEELGHRDVAR 120  
 Db 61 epncadpatltrpvhdaregflldtlvvlragnarldvdmgrlpvdlaeeelghrdvar 120  
 OY 121 YLRRAAGCTGSGNHARIDAAEGPSDIPD 148  
 Db 121 ylrraagctrgsnharidaaegpsdipd 148

RESULT 2  
 AAR80940  
 ID AAR80940 standard; Protein; 148 AA.  
 XX  
 AC AAR80940;  
 XX  
 DT 03-MAY-1996 (first entry)  
 XX  
 DE Human multiple tumour suppressor polypeptide, MTS1.  
 XX  
 KM Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;  
 KM astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;  
 KM gene therapy; chronic.

XX Homo sapiens.  
 PN WO9525429-A1.  
 XX  
 PD 28-SEP-1995.  
 XX  
 PF 17-MAR-1995; 95WO-US03316.  
 XX  
 PR 01-JUN-1994; 94US-0251938.  
 PR 18-MAR-1994; 94US-0214581.  
 PR 18-MAR-1994; 94US-0214582.  
 PR 18-MAR-1994; 94US-0215088.  
 PR 14-APR-1994; 94US-0227369.  
 PR 18-MAR-1994; 94US-0215086.  
 PR 18-MAR-1994; 94US-0215087.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.  
 XX  
 PI Kamb A;  
 XX  
 DR WPI: 1995-344401/44.  
 DR N-PSDB: AAO99158.  
 XX

PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences  
 PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.  
 PT melanoma or leukaemia  
 XX  
 PS Claim 5; Page 92-93; 156pp; English.  
 XX

CC Several multiple tumour suppressor (MTS) polypeptides have been  
 CC isolated and sequenced. This sequence is the MTS polypeptide MTS1  
 CC MTS polypeptide-encoding cDNAs and mutants of these are useful for  
 CC the diagnosis or prognosis of human cancer. Germ-line mutations of  
 CC MTS cDNAs can be used for diagnosing predisposition to melanoma,  
 CC leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's  
 CC lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus,  
 CC testis, kidney, stomach and rectum. The wild-type gene is useful  
 CC for gene therapy and MTS polypeptides may also be used for protein  
 CC replacement therapy. Also the polypeptides or cells contg. an  
 CC altered MTS gene are useful for screening for potential cancer  
 CC therapeutics.  
 CC  
 XX Sequence 148 AA:  
 SQ

Query Match 100.0%; Score 760; DB 16; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 6,6e-83;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEPSADWLATAARGVEEVRALLEAVALPNAPNSYGRPRIOYMMGASARVAELLHGA 60  
 Db 1 mepsadwlataaargveevrallleavalpnapsygrpridyvmngsarvaeilllhga 60  
 OY 61 EPNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVDMGRLPVDLAEEELGHRDVAR 120  
 Db 61 epncadpatltrpvhdaregflldtlvvlragnarldvdmgrlpvdlaeeelghrdvar 120  
 OY 121 YLRRAAGCTGSGNHARIDAAEGPSDIPD 148  
 Db 121 ylrraagctrgsnharidaaegpsdipd 148

RESULT 3  
 AAR53401  
 ID AAR53401 standard; Protein; 151 AA.  
 XX  
 AC AAR53401;  
 XX  
 DT 07-DEC-1994 (first entry)  
 XX  
 DE Inhibitor of cyclin dependent kinase 4 (p16INK4).  
 XX  
 KM Cyclin; cyclin dependent kinase; CDK; oncogene; cancer; leukaemia;  
 KM lymphoma; cell cycle; detection; identification; tumour virus;  
 KM proliferating cell nuclear antigen; subunit; complex.  
 XX  
 OS Homo sapiens.  
 PN WO9409135-A.  
 XX  
 PD 28-APR-1994.  
 XX  
 PF 18-OCT-1993; 93WO-US09945.  
 XX  
 PR 16-OCT-1992; 92US-0963308.  
 PR 17-DEC-1992; 92US-0991997.  
 XX  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 XX  
 PI Beach DH, Xiong Y;  
 XX  
 DR WPI: 1994-151320/18.  
 DR N-PSDB: AAO63491.  
 XX  
 PT Detection of subunit components of cyclin complexes - used for  
 PT diagnosing transformation of a cell and developing inhibitors and

PT activators, partic for cancer treatment  
 XX  
 PS Claim 13; Page 40; 45pp; English.  
 XX  
 CC The cell cycle gene implicated most strongly in oncogenesis is the  
 CC human cyclin D1. It is genetically linked to the bcl-1 oncogene, a  
 CC locus activated by translocation to an immunoglobulin gene enhancer  
 CC in some B-cell lymphomas and leukemias. D-type cyclin, cyclin  
 CC dependant kinase (CDK), PCNA (proliferating cell nuclear antigen) and  
 CC p21 (a 21 kDa polypeptide) exist in a quaternary complex that many  
 CC combinatorial variations of the components e.g. cyclin D1 or D3 and  
 CC CDK2, CDK4 and CDK5, assemble in vivo. Each quaternary complex may  
 CC have a subtly different role in the cell cycle or in different cell  
 CC types. Cellular transformation by DNA tumour viruses such as SV40  
 CC is associated with selective subunit rearrangement of the cyclin D  
 CC complexes. In virally transformed cells, CDK4 totally dissociates  
 CC from cyclin, PCNA and p21 and becomes associated with a 16 kilodalton  
 CC polypeptide (p16). This sequence, designated p16INK4, binds to and  
 CC inhibits CDK4. p16INK4 was discovered to show many similarities to  
 CC p16. Reagents, such as monoclonal antibodies, can be developed that  
 CC recognise the interactions between the CDK's cyclins, PCNA and low  
 CC molecular weight polypeptides and can therefore be used to identify  
 CC the state of transformation of a cell.  
 CC  
 SQ Sequence 151 AA;  
 Query Match 100.0%; Score 760; DB 15; Length 151;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-83;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEPSADWLATAAARGVEEVRALLLEAVALPNAAPNSYGRPRPQVMMGSAARVAELLHLHGA 60  
 Db 1 mepsadwlataaargveevrallleavallpnapsygrprpqvmmgsarvaeellllhga 60  
 QY 61 EPNCADPATLTRPVHDAAREGFLDTLVTLHRAGARLDVRDAGRLPVDLAELGHRDVAR 120  
 Db 61 epncadpatltrpvhdaaeregflidtlvhlragarldvrdagrlpvdlaeelghrdvar 120  
 QY 121 YLRAAAGTGRGSHARIDAEGSPDIPD 148  
 Db 121 ylr aaagtgrgsharidaegspdipd 148  
 RESULT 4  
 AAR85116  
 ID AAR85116 standard; Protein; 156 AA.  
 XX  
 XX AAR85116;  
 DT 01-MAR-1996 (first entry)  
 DE Cell-cycle regulatory protein p16.  
 DE Cell-cycle regulatory protein p16.  
 KW Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;  
 KW CCR; cancer; cell proliferation.  
 XX  
 OS Homo sapiens.  
 PN M09528483-A1.  
 PD 26-OCT-1995.  
 PF 14-APR-1995; 95WO-US04636.  
 PR 29-NOV-1994; 94US-0346147.  
 PR 14-APR-1994; 94US-0227371.  
 PR 25-MAY-1994; 94US-0248812.  
 PR 14-SEP-1994; 94US-0306511.  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 PI Beach DH, Demetrick DJ, Hannon GT, Serrano M;

XX  
 DR WPI; 1995-373798/48.  
 DR N-PSDB; AAT02962.  
 XX  
 PT New cell cycle regulating proteins bind to cyclin dependent kinase  
 PT and related nucleic acids, antibodies etc., used in diagnosis and  
 PT therapy of abnormal cell proliferation, degeneration etc.  
 XX  
 PS Claim 1; Page 76-77; 109pp; English.  
 XX  
 CC The human cell-cycle regulatory (CCR) protein p16 (AAR85116) was  
 CC obtd. by expression of a cDNA clone (AAT02962) isolated in a 2-hybrid  
 CC screening assay. CCR p16 specifically inhibits the activity of  
 CC cyclin-dependent kinases during various stages of the cell cycle,  
 CC and can be used in the treatment and diagnosis of proliferative  
 CC disorders.  
 CC  
 SQ Sequence 156 AA;  
 Query Match 100.0%; Score 760; DB 16; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-83;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEPSADWLATAAARGVEEVRALLLEAVALPNAAPNSYGRPRPQVMMGSAARVAELLHLHGA 60  
 Db 9 mepsadwlataaargveevrallleavallpnapsygrprpqvmmgsarvaeellllhga 68  
 QY 61 EPNCADPATLTRPVHDAAREGFLDTLVTLHRAGARLDVRDAGRLPVDLAELGHRDVAR 120  
 Db 69 epncadpatltrpvhdaaeregflidtlvhlragarldvrdagrlpvdlaeelghrdvar 128  
 QY 121 YLRAAAGTGRGSHARIDAEGSPDIPD 148  
 Db 129 ylr aaagtgrgsharidaegspdipd 156  
 RESULT 5  
 AAY24741  
 ID AAY24741 standard; Protein; 156 AA.  
 XX  
 XX AAY24741;  
 DT 23-AUG-1999 (first entry)  
 DE Human INK-4 protein p16.  
 DE INK-4; p16; p15; p18; p19; CDK4; cell cycle regulatory protein;  
 KW transgenic mouse; p16-INK4-a; carcinogen; anti-proliferative.  
 XX  
 OS Homo sapiens.  
 PN US5919997-A.  
 PD 06-JUL-1999.  
 PF 04-APR-1996; 96US-0627610.  
 PR 04-APR-1996; 96US-0627610.  
 PR 18-NOV-1993; 93US-0154915.  
 PR 14-APR-1994; 94US-0227371.  
 PR 25-MAY-1994; 94US-0248812.  
 PR 14-SEP-1994; 94US-0306511.  
 PR 29-NOV-1994; 94US-0346147.  
 PR 30-JUN-1995; 95US-0497214.  
 PR 02-JAN-1996; 96US-0581918.  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.  
 PI Beach DH, Depinho RA, Serrano M;  
 WPI; 1999-394656/33.

DR N-PSDB: AAX80472.  
 XX Transgenic mice with modified cell-cycle regulation  
 PT Disclosure; Column 45-46; 35pp; English.  
 XX  
 PS The present invention describes a transgenic mouse having germline and  
 CC somatic cells which comprise an incorporated transgene that disrupts and  
 CC inhibits the p16-INK4-a gene leading to tumour susceptibility. Also  
 CC described is a method of making a mouse and mouse embryonic stem cells a  
 CC functionally disrupted p16-INK4-a gene which comprises transferring a  
 CC transgene construct into embryonic stem cells of a mouse and  
 CC transferring these into a mouse blastocyst and implanting the resulting  
 CC chimeric blastocyst into a female mouse selecting offspring having an  
 CC endogenous p16-INK4-a gene allele. The transgenic mouse is useful for  
 CC evaluating the carcinogenic potential or the anti-proliferative activity  
 CC of a test compound. The present sequence represents the human INK4  
 CC protein p16 given in the present invention.  
 CC  
 XX Sequence 156 AA;  
 SO  
 Query Match 100.0%; Score 760; DB 20; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-83;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEPSADWLTATTAAGRVEEVRALLLEAVALPNAPNSYGRPIQVMMGSAFVALLLHGA 60  
 DB 9 mepsadwltatargveevrallleavallpnapsygrpdyqmmngsarvae111llhga 68  
 QY 61 EPNCADPATLTTPVHDAAREGFLDTLVVLRAGARLDVDRAGRLPVDLAEEIGHRDVAR 120  
 DB 69 epcncaadpatlttrpyhdaaregflidtlvvlrhagariidvdawgrlpvdlaeelghrdvar 128  
 QY 121 YLRAAAGCTRGSNHARIDAAEGPSDIPD 148  
 DB 129 yllraaagctrgsnharidaaegpsdipd 156  
 RESULT 6  
 AAX8354  
 ID AAX8354 standard; Protein: 156 AA.  
 XX  
 AC AAX8354;  
 XX  
 DT 14-JUL-2000 (first entry)  
 XX  
 DE Human cell cycle regulatory protein p16 amino acid sequence.  
 KM Cell cycle regulatory protein; CCR; p16; diagnostic assay; detection;  
 XX cyclin-dependent kinase inhibitor; CDK; human; chromosome 9p21-22.  
 OS Homo sapiens.  
 XX  
 PN US6043030-A.  
 XX  
 PD 28-MAR-2000.  
 XX  
 PF 02-JAN-1996; 96US-0581918.  
 XX  
 PR 17-DEC-1992; 92US-0991997.  
 PR 18-NOV-1993; 93US-0154915.  
 PR 14-APR-1994; 94US-0227371.  
 PR 25-MAY-1994; 94US-0248812.  
 PR 14-SEP-1994; 94US-0306511.  
 PR 29-NOV-1994; 94US-0346147.  
 PR 30-JUN-1995; 95US-0497214.  
 XX  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 XX  
 PI Beach DH, Demetrick DJ, Serrano M, Hannon GJ;  
 XX

DR WPI: 2000-270336/23.  
 DR N-PSDB: AAA13096.  
 XX  
 PT Use of a mammalian cell cycle regulatory protein (a CDK-inhibitory  
 PT protein) in a diagnostic assay for identifying a cell at risk for a  
 PT disorder characterized by unwanted cell proliferation or  
 PT differentiation -  
 XX  
 PS Claim 14; Column 57-58; 61pp; English.  
 XX  
 CC This sequence represents the human cell cycle regulatory protein (CCR)  
 CC p16 amino acid sequence. The p16 gene is located on chromosome 9p21-22.  
 CC The invention relates to a diagnostic assay which comprises detecting a  
 CC mutation in the p16 gene, which is used to identify a cell or cells at  
 CC risk of developing a disorder characterised by unwanted cell  
 CC proliferation or differentiation. p16 is a cyclin-dependent kinase  
 CC (CDK)-inhibitory protein, and functions as an inhibitor of cell-cycle  
 CC progression and ultimately cell growth. The assay can be used for  
 CC identifying a cell or cells at risk for a disorder (neoplasia)  
 CC characterized by unwanted cell proliferation or differentiation. The  
 CC method is used for detecting mutations in either a CCR gene or CDK gene  
 CC which alter complex formation between these two proteins. The method is  
 CC also used for detecting mutations in other cellular proteins which  
 CC disrupt protein interactions such as mutations which disrupt binding of  
 CC the p53 protein with other cellular proteins, e.g. Wilm's tumour  
 CC suppressor protein WT1. They can also be used to detect mutations in  
 CC pairs of signal transduction proteins such as ras protein or other  
 CC cellular proteins which interact with ras, e.g. ras GTPase activating  
 CC proteins (GAPs). The method is convenient for detecting mutants of CCR  
 CC genes encoding proteins which are unable to physically interact with a  
 CC CDK bait protein.  
 CC  
 XX Sequence 156 AA;  
 SO  
 Query Match 100.0%; Score 760; DB 21; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-83;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEPSADWLTATTAAGRVEEVRALLLEAVALPNAPNSYGRPIQVMMGSAFVALLLHGA 60  
 DB 9 mepsadwltatargveevrallleavallpnapsygrpdyqmmngsarvae111llhga 68  
 QY 61 EPNCADPATLTTPVHDAAREGFLDTLVVLRAGARLDVDRAGRLPVDLAEEIGHRDVAR 120  
 DB 69 epcncaadpatlttrpyhdaaregflidtlvvlrhagariidvdawgrlpvdlaeelghrdvar 128  
 QY 121 YLRAAAGCTRGSNHARIDAAEGPSDIPD 148  
 DB 129 yllraaagctrgsnharidaaegpsdipd 156  
 RESULT 7  
 AAX23534  
 ID AAX23534 standard; Protein: 391 AA.  
 XX  
 AC AAX23534;  
 XX  
 DT 16-MAR-1998 (first entry)  
 XX  
 DE CDK inhibitory fusion protein #1.  
 XX  
 KW Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gene;  
 KW chimeric polypeptide; human; binding motif; proliferation control;  
 KW cell differentiation; cell-cycle inhibitor; proliferative disorder;  
 KW tissue degeneration; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1..7  
 FT /note="poly-His tag"  
 FT Misc-difference 205..219



```

XT      /note= "(GlySer)2 linker"
XX      PN      WO9727297-A1.
XX      PD      31-JUL-1997.
XX      PE      17-JAN-1997; 97WO-US00569.
XX      PR      23-JAN-1996; 96US-0589981.
XX      PA      (MITO-) MITOTIX INC.
XX      PI      Beach D, Gyuris J, Lamphere L;
XX      DR      WPI: 1997-3393685/36.
XX      DR      N-PSDB: MAT74051.
XX      PT      Chimeric inhibitor of cyclin dependent kinase - useful for gene
XX      PT      therapy of cancer and other proliferative and differentiative
XX      PT      diseases
XX      P1      Claim 40; Page 38-40; 58pp; English.
XX      P2      This sequence represents a chimeric polypeptide of the invention. It was
XX      P3      derived from a fusion of the human p27 and p16 cDNA sequences. The
XX      P4      chimeric polypeptides of the invention have cyclin-dependent kinase (CDK)
XX      P5      binding motifs from at least two different proteins that bind to CDKs.
XX      P6      The protein controls proliferation and/or differentiation of cells,
XX      P7      particularly they inhibit cell-cycle progression. They can be used to
XX      P8      treat a wide range of proliferative disorders, e.g. cancer, leukaemia,
XX      P9      psoriasis, atherosclerosis, stenosis, chronic inflammation etc. They
XX      P10     can also treat diseases associated with de-differentiation or
XX      P11     degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's
XX      P12     disease, gastric ulcers and autonomous diseases of the peripheral
XX      P13     nervous system. Other applications include reducing growth of hair and
XX      P14     protecting hair follicle cells against cytotoxic treatments, cosmetically
XX      P15     to treat various forms of folliculitis, and to inhibit spermatogenesis or
XX      P16     oogenesis. The chimeric proteins can also be used in vitro to maintain
XX      P17     cells, especially neurons intended for testing specific activity of
XX      P18     trophic factors, at selected points in the cell cycle. The proteins are
XX      P19     more active inhibitors of the CDK/cyclin complex than binding motifs used
XX      P20     individually (since they may bind to CDK involved in different stages of
XX      P21     the cell cycle).
XX      SQ      Sequence 391 AA:
XX
XX      Query Match 100.0%; Score 760; DB 18; Length 391;
XX      Local Similarity 100.0%; Pred. No. 2,4e-82;
XX      Chex 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX      QY      1 MEPSADMTLTAARGRVEEVALLLEAVLPNAPNSYGRPIQVMMGSRVAFLELLHGA 60
XX      DB      244 mepsadwtlaaargveeviralleaalpnapnsygrp1qvmungsarvae111111hga 303
XX      QY      61 EPNCADPATLTTPVHHAAEEGFLLDTLVVLRHAGARLDVDVDMQRLPVDLAEEIGHRDVAR 120
XX      DB      304 epcncaapatlttvpvhaaeegflldtlvvlnrgharldvdaagripvdlaeeighrdvar 363
XX      QY      121 YLRAAAGTGRGSNHARIDAEEGPSDIPD 148
XX      DB      364 ylraaagtrgsnharidaaegpsdipd 391
XX
XX      RESULT 8
XX      ID      AAW95094
XX      AC      AAW95094;
XX      DT      25-MAY-1999 (first entry)
XX      DE      Human p27-p16 fusion protein.

```

XX Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;  
KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;  
KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;  
KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;  
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;  
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;  
KW tachycardia; human; p27; p16.  
XX  
OS Homo sapiens.  
XX  
FN WO9906540-A2.  
XX  
PD 11-FEB-1999.  
XX  
PF 29-JUL-1998; 98WO-US15759.  
XX  
PR 29-JUL-1997; 97US-0902572.  
XX  
PA (MITO-) MITOTIX INC.  
XX  
Beach DH, Gyuris J, Lamphere L;  
DR WPI: 1999-153770/L3.  
XX N-PESDB; AAX26220.  
XX  
PT Fusion and chimaeric proteins including cyclin-dependent kinase  
PT binding motif - used for regulation of cell proliferation and  
PT differentiation, for treatment of, e.g. vascular injury, cancers,  
PT fibrosis and neurodegeneration  
XX  
PS Claim 63; Page 70-72; 88pp; English.  
XX  
XX The invention relates to novel inhibitors of cyclin-dependent kinases  
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant  
CC transfection system (A) that comprises: (i) first gene construct  
CC comprising a sequence encoding an inhibitory polypeptide containing at  
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,  
CC linked to a transcription regulator functional in eukaryotic cells; (ii)  
CC second gene construct comprising a sequence encoding a polypeptide that  
CC promotes endothelialisation, and (iii) a gene delivery composition for  
CC delivering the Gcs to a cell for transfection. Also provided are nucleic  
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic  
CC polypeptide sequence (TP) from an intracellular protein that alters a  
CC cellular process when FP enters the cell, and (ii) a transcellular  
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP  
CC consists of at least one CDK-binding motif and a TCP. (A) are used to  
CC treat vascular wounds that involve a break in the endothelium and  
CC excessive proliferation of smooth muscle, particularly restenosis but  
CC more generally any repair of cardiovascular damage, arteriosclerotic  
CC lesions or for endothelialisation of synthetic vascular grafts. More  
CC generally, FP are used to treat unwanted cellular proliferation in a very  
CC wide range of situations, e.g. for treating vascular diseases as above;  
CC fibrotic disorders (e.g. rheumatoid arthritis, diabetes, cirrhosis); many  
CC tumours (gliomas, leukaemias); chronic inflammation; neurodegeneration,  
CC acne; also to control hair growth (e.g. to prevent hair loss caused by  
CC chemotherapy or radiation); periodontal disease; to treat tachycardia;  
CC to inhibit spermatogenesis etc. Chimaeric proteins comprising CDK-binding  
CC motifs from two or more different proteins bind to CDKs so inhibit cell  
CC cycle progression, particularly smooth muscle cell proliferation. The  
CC gene constructs may also be used to produce FP in cell cultures, for  
CC production or for regulating cell differentiation *in vitro*. The present  
CC sequence represents a human p27-p16 fusion protein.  
XX  
SO Sequence 391 AA:

Query Match 100.0%; Score 760; DB 20; Length 391;  
Best Local Similarity 100.0%; Pred. No. 2.4e-82;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

1 MEMSDMLAAARGREEVRALEVALPMANNSGRRPQVMAGGSARVAELLHLGA 60  
|||||

Db 244 mepsadwlatataargveevraalleavalpnapsygrripqymmgasarvae11llhga 303  
 Oy 61 EPNCADPATLTRPVHDAAREGFLDTLVLRAGARLDVBDAMGRLLPVDLAEEIGHRDVAR 120  
 |||||||  
 Db 304 epnacadpatltrpvhdaaregflidtlvlhregarldvrdaawgrlpvdlaeelghrdvar 363  
 Oy 121 YLRAAGTGRGSHARIDAAEGPSDIPD 148  
 |||||||  
 Db 364 ylraaagtrgsnharidaaegpsdipd 391

## RESULT 9

AA97526  
 ID AAY97526 standard; Protein; 391 AA.

XX AAY97526;

XX 15-JAN-2001 (first entry)

XX Human W3 protein sequence.

Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;  
 adenovirus E4 protein; neoplasia; W3 protein.

XX Homo sapiens.

XX WO200052184-A1.

XX 08-SEP-2000.

XX 01-MAR-2000; 2000WO-US05350.

XX 01-MAR-1999; 99US-0122974.

XX 08-APR-1999; 99US-0128271.

XX 09-APR-1999; 99US-0128515.

XX (CELL-) CELL GENESYS INC.

XX (MITO-) MITOTIX INC.

XX Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;

XX WPI: 2000-587315/55.

XX N-PSDB: AAA90923.

XX Example 1; Page 108-109; 126pp; English.

XX This sequence represents the human W3 protein.

XX The invention relates to a protein composition comprising a novel

XX purified chimeric cyclin dependent kinase inhibitor (CDK1) and a

XX purified adenovirus E4 protein. The compositions comprising the protein,

XX or the DNA encoding it are useful for treating neoplasias in animals. The

XX compositions also find use in assays to eliminate a specific

XX sub-population of cultured cells, to determine the susceptibility of

XX neoplastic cells to treatment with the compositions and also in assays to

XX synchronize cell growth in cultured cells.

XX Sequence 391 AA;

XX

Oy 1 MEPSADWLATAARGVEEVRAALLEAVALPNAPNSYGRRIQYMMNGSARVAELLLHGA 60  
 |||||||  
 Db 244 mepsadwlatataargveevraalleavalpnapsygrripqymmgasarvae11llhga 303  
 |||||||  
 Oy 61 EPNCADPATLTRPVHDAAREGFLDTLVLRAGARLDVBDAMGRLLPVDLAEEIGHRDVAR 120  
 |||||||

Db 304 epnacadpatltrpvhdaaregflidtlvlhregarldvrdaawgrlpvdlaeelghrdvar 363  
 Oy 121 YLRAAGTGRGSHARIDAAEGPSDIPD 148  
 |||||||  
 Db 364 ylraaagtrgsnharidaaegpsdipd 391

## RESULT 10

AA96041  
 ID AAY96041 standard; Protein; 391 AA.

XX AAY96041;

XX 05-DEC-2000 (first entry)

XX Antiproliferative p27-p16 fusion protein W3.

XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; p27; INK4;

XX p16; human; smooth muscle cell; hyperproliferation; restenosis;

XX vasotropic; antiproliferative; gene therapy.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX Peptide 1..7

XX Protein /label= 6His\_tag

XX Peptide 205..219

XX Protein /label= Hinge

XX WO200052159-A1.

XX 08-SEP-2000.

XX 28-FEB-2000; 2000WO-US04971.

XX 01-MAR-1999; 99US-0122974.

XX 05-NOV-1999; 99US-0163682.

XX 09-DEC-1999; 99US-0457568.

XX (CELL-) CELL GENESYS INC.

XX (MITO-) MITOTIX INC.

XX McArthur J, Gyuris J, Finer M;

XX WPI: 2000-594183/56.

XX N-PSDB: AAA50488.

XX Novel recombinant lentivirus for inhibiting proliferation of smooth

XX muscle cells in e.g. restenosis, is replication deficient and comprises

XX a transgene encoding a cyclin dependent kinase inhibitor -

XX Example 1; Page 101-103; 126pp; English.

XX The present sequence is that of p27-p16 fusion protein W3 comprising

XX an N-terminal 6His tag, the human p27 protein (see AAY96052), a

XX (GlySer)3 hinge and the human p16 protein (see AAY96053). It is

XX encoded by a nucleic acid obtained by PCR amplification of p27 and

XX p16 DNAs using primers that also included codons for the tag/hinge

XX regions. A claimed method for inhibiting smooth muscle cell

XX hyperproliferation involves transducing smooth muscle cells with a

XX replication-deficient recombinant adenovirus that lacks functional

XX E1 and E4 regions, and comprises a transgene encoding a cyclin

XX dependent kinase inhibitor (CDK1). The CDK1 is selected from an

XX INK4 family protein such as human p16, a CIP/KIP family protein

XX such as p27, active fragments of these, or fusion proteins

XX comprising (active fragments of) an INK4 family protein and a

XX CIP/KIP family protein (see AAY96046 and AAY96049). The method is used

XX to inhibit mammalian smooth muscle cell hyperproliferation, induced

CC by injury caused by angioplasty, stent placement or vein  
CC engraftment. It is useful for treating vascular pathologies e.g.,  
CC restenosis. Also claimed are recombinant lentiviruses encoding  
CC CDKs.

XX Sequence 391 AA:

Query Match 100.0%; Score 760; DB 21; Length 391;  
Best Local Similarity 100.0%; Pred. No. 2,4e-82;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLTAAAGRVEVRALLPAPNSYGRPIQVMMGSAFYAEILLHGA 60  
DB 244 mepsadwltaaargveevrallpnapnsygrripqymmsarvaeillllhga 303  
QY 61 EPNCADPATITRPVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAEELGHRDYAR 120  
DB 304 epncadpatlitrpvhdaaregfldtlvvlrhagardvrdawgrlpvdlaeelghrdvar 363  
Q 121 YLRAAAGTGRGSHARIDAEGPSDIPD 148  
DB 364 ylraaagtrgsharidaegpsdipd 391

RESULT 11

AA96068  
ID AAY96068 standard; Protein; 391 AA.

AC AAY96068;

DT 05-DEC-2000 (first entry)

DE Angiogenesis inhibitor (p27-p16 fusion) W3.

XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; INK4; p27; p16;  
KW human; angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;  
KW endometriosis; psoriasis; vascular retinopathy; cytostatic;  
KW antirheumatic; antineumatic; gynaecological; antiproliferative;  
KW antiproliferative; gene therapy.

XX OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

EH Peptide 1..7 /label= 6His\_tag

FT Protein 8..204 /label= p27

FT Peptide 205..219 /label= p16

FT Peptide 239..391 /label= p16

FT Protein /label= p16

FT Protein /label= p16

XX WO200052158-A1.

XX 08-SEP-2000.

XX 28-FEB-2000; 2000WO-US04970.

XX 01-MAR-1999; 99US-0122974.

XX 05-NOV-1999; 99US-0163682.

XX 09-DEC-1999; 99US-0457646.

XX (CELL-) CELL GENESYS INC.

XX (MITO-) MITOTIX INC.

XX Patel S, Marchur J, Gyuris J;

XX WPI; 2000-565501/52.

XX N-PSDB; AAA50523.

XX Inhibiting angiogenesis and treating angiogenesis-associated

PT conditions, e.g. neoplasia, psoriasis by transducing an endothelial  
PT cell with a recombinant virus having a transgene encoding a cyclin  
PT dependent kinase inhibitor

XX Example 1; Page 108-110; 138pp; English.

CC The present sequence is that of p27-p16 fusion protein W3  
CC comprising an N-terminal 6His tag, the human p27 protein (see  
CC AAY96066), a (GlySer)3 hinge, and the human p16 protein (see  
CC AAY96067). The fusion protein is encoded by a nucleic acid (see  
CC AAA50523) that was obtained by PCR amplification of human p27 and p16  
CC DNAs using primers that also included codons encoding the tag/hinge  
CC regions of the fusion protein. A claimed method for inhibiting  
CC angiogenesis involves transducing an epithelial cell with a  
CC transgene encoding a cell dependent kinase inhibitor (CDK1). The  
CC delivery system for the transgene is a liposome or a recombinant  
CC virus. The CDK1 is a protein of the CIP/KIP family such as p27, a  
CC protein of the INK4 family such as p16, active fragments of these  
CC proteins, or a fusion of 2 CDK1 proteins such as p27 and p16. The  
CC method is useful in treating conditions associated with angiogenesis,  
CC such as neoplasia, rheumatoid arthritis, endometriosis, psoriasis  
CC and vascular retinopathy (claimed). Alternatively, the transgene  
CC is delivered to an auxiliary cell, and is expressed by that cell  
CC such that the CDK1 is released into the blood and contacts the  
CC target epithelial cell. The p27-p16 fusion proteins interact with  
CC CDK4/cyclinD, CDK2/cyclinA and CDK2/cyclinE and inhibit cell cycle  
CC progression.

XX Sequence 391 AA:

Query Match 100.0%; Score 760; DB 21; Length 391;  
Best Local Similarity 100.0%; Pred. No. 2,4e-82;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLTAAAGRVEVRALLPAPNSYGRPIQVMMGSAFYAEILLHGA 60  
DB 244 mepsadwltaaargveevrallpnapnsygrripqymmsarvaeillllhga 303  
QY 61 EPNCADPATITRPVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAEELGHRDYAR 120  
DB 304 epncadpatlitrpvhdaaregfldtlvvlrhagardvrdawgrlpvdlaeelghrdvar 363  
QY 121 YLRAAAGTGRGSHARIDAEGPSDIPD 148  
DB 364 ylraaagtrgsharidaegpsdipd 391

RESULT 12

AAW10627  
ID AAW10627 standard; Protein; 156 AA.

AC AAW10627;

DT 28-OCT-1997 (first entry)

DE Tumour suppressor p16.

XX Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;

XX cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;

XX anti-angiogenic activity; hyperproliferative disorder.

XX Homo sapiens.

XX WO9703635-A2.

XX 06-FEB-1997.

XX 17-JUL-1996; 96WO-US11787.

XX 17-JUL-1995; 95US-0502881.

XX (TEXA ) UNIV TEXAS SYSTEM.

```

XX  Jln X, Roth J;
PI
XX
XX  WPI: 1997-132336/12.
DR  N-PSDB; AAT60951.
XX
XX  Expression construct contg. DNA for tumour suppressor p16 - to
PT  restore p16 activity to transformed cells, useful for treating lung
PT  or bladder cancer or melanoma
XX
XX  Disclosure; Fig 1b; 92pp; English.
XX
CC  This sequence represents the tumour suppressor p16. The DNA encoding
CC  this sequence is joined to a promoter functional in eukaryotic cells and
CC  used in the expression construct of the invention. p16 is an inhibitory
CC  subunit, which is involved in the control of cyclin-dependent kinase 4
CC  activity, and functions as a tumour suppressor. By detecting this
CC  sequence or the DNA encoding it, cancer cells can be detected. When the
CC  nucleic acid molecule is in the sense orientation, the expression
CC  construct can be used to restore p16 function in a cell, particularly by
CC  reversing the transformed phenotype in tumours, especially lung or
CC  bladder cancer or melanoma. It may also have anti-angiogenic activity,
CC  and inhibit hyperproliferative disorders, e.g. restenosis. When the
CC  nucleic acid molecule is inserted in the antisense orientation, the
CC  expression construct inhibits p16 function. Reduced or increased levels
CC  of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by
CC  Southern or Northern blot, antibody immunoblot, fluorescent cell sorting
CC  or immunoassay.
XX
SQ  Sequence 156 AA;

Query Match 99.1%; Score 753; DB 18; Length 156;
Best Local Similarity 99.3%; Pred. No. 4.9e-82;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MESPADWLATAARGRVEEVRALLEAVLFPNAPNSYGRPIQVMGSAVAELLHLHGA 60
DB 9 mepsadwlataaargveevrallleagalpnapnsygrpipyvmngsarvaellllhga 68

OY 61 EPNCADPATLTTPRVHDARREGFLDTLVVLRAGARLDVDRMGRLPVDAEELGHRDVAR 120
DB 69 epcncaapatlttrpyhdareregfltdltvvlhragarldvdrwgrlpvdaeeighrdvar 128

OY 121 YLRAAAGTGRGSHNARIDAAEGPSDIPD 148
DB 129 ylraaaagtgtrgshnaridaaegpsdipd 156

RESULT 13
AAW19251
ID AAW19251 standard; Protein; 156 AA.
XX
XX  AAW19251;
XX
XX  10-SEP-1997 (first entry)
XX
DE Human multiple tumour suppressor 1 gene product.
XX
XX Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis.
XX
OS Homo sapiens.
XX
XX US5624819-A.
XX
XX 29-APR-1997.
XX
XX 18-MAR-1994; 94US-0214582.
XX
XX 07-JUN-1995; 95US-0474177.
XX
XX 18-MAR-1994; 94US-0214582.
XX
XX 18-MAR-1994; 94US-0215086.
XX
XX 18-MAR-1994; 94US-0215087.

```

```

PR 14-APR-1994; 94US-0227369.
PR 01-JUN-1994; 94US-0251938.
PR 17-MAR-1995; 95WO-0503537.
XX
XX (MYRI-) MYRIAD GENETICS INC.
PA (UTAH) UNIV UTAH RES FOUND.
PI Cannon-Albright LA, Kamb A, Skolnick MH;
XX
XX WPI: 1997-258217/23.
DR N-PSDB; AAT72311.
XX
XX Human mutant multiple tumour suppressor gene sequences - for
PT production of recombinant mutant polypeptide(s)
XX
XX Claim 1; Columns 61-64; 72pp; English.
XX
XX The present sequence the human multiple tumour suppressor 1
CC (MTS1) gene product, useful in cancer diagnosis.
CC
XX
SQ Sequence 156 AA;

Query Match 99.1%; Score 753; DB 18; Length 156;
Best Local Similarity 99.3%; Pred. No. 4.9e-82;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MESPADWLATAARGRVEEVRALLEAVLFPNAPNSYGRPIQVMGSAVAELLHLHGA 60
DB 9 mepsadwlataaargveevrallleagalpnapnsygrpipyvmngsarvaellllhga 68

OY 61 EPNCADPATLTTPRVHDARREGFLDTLVVLRAGARLDVDRMGRLPVDAEELGHRDVAR 120
DB 69 epcncaapatlttrpyhdareregfltdltvvlhragarldvdrwgrlpvdaeeighrdvar 128

OY 121 YLRAAAGTGRGSHNARIDAAEGPSDIPD 148
DB 129 ylraaaagtgtrgshnaridaaegpsdipd 156

RESULT 14
AAW74549
ID AAW74549 standard; Protein; 156 AA.
XX
XX  AAW74549;
XX
XX  04-DEC-1998 (first entry)
XX
XX Amino acid sequence of multiple tumour suppressor 1.
DE Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
XX somatic mutation; gene therapy.
XX
XX
XX Homo sapiens.
XX
XX US5801236-A.
XX
XX 01-SEP-1998.
XX
XX 07-JUN-1995; 95US-0480810.
XX
XX 07-JUN-1995; 95US-0480810.
XX
XX 18-MAR-1994; 94US-0214582.
XX
XX 18-MAR-1994; 94US-0215086.
XX
XX 18-MAR-1994; 94US-0215087.
XX
XX 14-APR-1994; 94US-0227369.
XX
XX 01-JUN-1994; 94US-0251938.
XX
XX 17-MAR-1995; 95WO-US03316.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Kamb A;
XX
XX

```

DR WPI: 1998-494842/42.  
DR N-PSDB; AAV53819.  
XX  
XX  
PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -  
PT useful as hybridisation probes, primers and recombinant production  
PT of MTS in the diagnosis and treatment of cancers related to MTS  
PT mutation(s)  
XX  
PS Disclosure; Column 63-64; 73pp; English.  
XX  
XX This is the amino acid sequence of the multiple tumour suppressor 1  
CC (MTS-1) protein, used in the method of the invention. The MTS gene  
CC is useful in the diagnosis and prognosis of human cancer, e.g. by  
CC standard nucleic acid hybridisation techniques, of patient samples. The  
CC mutated sequences are those that are present in somatic mutations  
CC of the gene in cancers. The vectors can be used for gene therapy  
CC strategies to replace function of mutated protein in patients. These  
CC can also be used to construct protein mimetics, also for therapeutic  
CC strategies. In addition the expression constructs can also be used  
CC for recombinant production of MTS. Recombinant MTS can be used to  
CC screen for drugs to be used for cancer therapy, and the protein  
CC itself may also be used to restore MTS function in a cell.  
XX  
SQ Sequence 156 AA:  
  
Query Match 99.1%; Score 753; DB 19; Length 156;  
Best Local Similarity 99.3%; Pred. No. 4.9e-82;  
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MESPADWLATAAARGVEVRALLLEAVLPNAPNSYGRPIQVMMGSAFYAELLHGA 60  
Db 9 mepsadwlataaargvevrallleagalpnapnsygrripqymmgssarvae1111hga 68  
QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDRAMGRPLVDLAELGHRDVAR 120  
Db 69 epncadpatltrpvhdaaregfldtlvvlhragarldvdrmgrlpydlaeelghrdvar 128  
QY 121 YLRAAGTGRGSHARIDAEGPSDIPD 148  
Db 129 ylr aaggtgrgsnharidaegpsdipd 156  
  
RESULT 15  
ID AAM40524  
XX AAM40524 standard; Protein; 156 AA.  
XX  
AC AAM40524;  
XX  
D 15-JUL-1998 (first entry)  
XX  
DE Human MTS1 protein.  
XX  
KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;  
KW familial melanoma locus; MLM; predisposition.  
XX  
OS Homo sapiens.  
XX  
PN US5739027-A.  
PD 14-APR-1998.  
XX  
PF 07-JUN-1995; 95US-0487033.  
XX  
PR 07-JUN-1995; 95US-0487033.  
PR 18-MAR-1994; 94US-0214582.  
PR 18-MAR-1994; 94US-0215086.  
PR 18-MAR-1994; 94US-0215087.  
PR 14-APR-1994; 94US-0227369.  
PR 01-JUN-1994; 94US-0251938.  
PR 17-MAR-1995; 95WO-0503316.  
XX  
PA (MYRI-) MYRIAD GENETICS INC.

XX  
PI Kamd A:  
XX  
DR WPI: 1998-250421/22.  
DR N-PSDB; AAV11238.  
XX  
XX  
PT DNA specific for Multiple Tumour Suppressor 161-beta gene - are  
PT useful for the diagnosis of cancers related to MTS1E1-beta  
PT mutation(s) and their treatment  
XX  
XX  
PS Disclosure; Column 63-64; 72pp; English.  
XX  
XX This sequence represents a human multiple tumour suppression protein,  
CC MTS1. The MTS gene locus is also referred to as the familial melanoma  
CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations  
CC in MTS genes can be used in the diagnosis of predisposition to cancers,  
CC e.g. melanoma, leukemia, astrocytoma, glioblastoma, lymphoma, glioma,  
CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,  
CC ovary, uterus, testis, kidney, stomach and rectum.  
XX  
SQ Sequence 156 AA:  
  
Query Match 99.1%; Score 753; DB 19; Length 156;  
Best Local Similarity 99.3%; Pred. No. 4.9e-82;  
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MESPADWLATAAARGVEVRALLLEAVLPNAPNSYGRPIQVMMGSAFYAELLHGA 60  
Db 9 mepsadwlataaargvevrallleagalpnapnsygrripqymmgssarvae1111hga 68  
QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDRAMGRPLVDLAELGHRDVAR 120  
Db 69 epncadpatltrpvhdaaregfldtlvvlhragarldvdrmgrlpydlaeelghrdvar 128  
QY 121 YLRAAGTGRGSHARIDAEGPSDIPD 148  
Db 129 ylr aaggtgrgsnharidaegpsdipd 156

Search completed: September 19, 2002, 17:23:40  
Job time: 39 sec



GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: September 19, 2002, 17:23:02 ; Search time 12.99 Seconds  
(without alignments)  
278.290 Million cell updates/sec

Title: US-09-016-869b-35  
Perfect score: 760  
Sequence: 1 MEPSADWLTAAARGVEEV.....TRGSNHRIDAEGPSDIPD 148

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	760	100.0	148	1 US-08-154-915-4	Sequence 4, Appl1
2	760	100.0	148	3 US-08-384-106A-16	Sequence 16, Appl1
3	760	100.0	148	3 US-08-384-106A-24	Sequence 24, Appl1
4	760	100.0	148	5 PCT-US93-09945-4	Sequence 4, Appl1
5	760	100.0	156	2 US-08-627-610-2	Sequence 2, Appl1
6	760	100.0	156	2 US-08-306-511A-2	Sequence 2, Appl1
7	760	100.0	156	2 US-08-893-274-2	Sequence 2, Appl1
8	760	100.0	156	2 US-08-581-918A-2	Sequence 2, Appl1
9	760	100.0	156	4 US-08-346-147B-2	Sequence 2, Appl1
10	760	100.0	156	4 US-08-822-936-2	Sequence 2, Appl1
11	760	100.0	156	5 PCT-US95-04636-2	Sequence 2, Appl1
12	760	100.0	391	1 US-08-589-981-2	Sequence 2, Appl1
13	753	99.1	156	1 US-08-474-177-2	Sequence 2, Appl1
14	753	99.1	156	1 US-08-487-033-2	Sequence 2, Appl1
15	753	99.1	156	1 US-08-480-810-2	Sequence 2, Appl1
16	753	99.1	156	2 US-08-508-735-2	Sequence 2, Appl1
17	753	99.1	156	2 US-08-848-251-2	Sequence 2, Appl1
18	753	99.1	156	2 US-08-486-047-2	Sequence 2, Appl1
19	753	99.1	156	3 US-09-120-130-2	Sequence 2, Appl1
20	753	99.1	156	3 US-09-115-252-2	Sequence 2, Appl1
21	753	99.1	156	3 US-08-986-515-2	Sequence 2, Appl1
22	753	99.1	156	4 US-09-120-128-2	Sequence 2, Appl1
23	753	99.1	156	4 US-09-120-129-2	Sequence 2, Appl1
24	753	99.1	156	4 US-09-201-139-2	Sequence 2, Appl1
25	753	99.1	156	4 US-09-120-131-2	Sequence 2, Appl1
26	753	99.1	156	4 US-08-910-722-2	Sequence 2, Appl1
27	749.5	98.6	157	5 PCT-US96-05252-5	Sequence 5, Appl1

28	627.5	82.6	157	3 US-08-581-918A-12	Sequence 12, Appl1
29	627.5	82.6	157	4 US-08-346-147B-12	Sequence 12, Appl1
30	544	71.6	105	1 US-08-474-177-14	Sequence 14, Appl1
31	544	71.6	105	1 US-08-487-033-14	Sequence 14, Appl1
32	544	71.6	105	1 US-08-480-810-14	Sequence 14, Appl1
33	544	71.6	105	2 US-08-508-735-14	Sequence 14, Appl1
34	544	71.6	105	2 US-08-848-251-14	Sequence 14, Appl1
35	544	71.6	105	2 US-08-486-047-14	Sequence 14, Appl1
36	544	71.6	105	3 US-09-120-130-14	Sequence 14, Appl1
37	544	71.6	105	3 US-09-115-252-14	Sequence 14, Appl1
38	544	71.6	105	3 US-08-986-515-14	Sequence 14, Appl1
39	544	71.6	105	4 US-09-120-128-14	Sequence 14, Appl1
40	544	71.6	105	4 US-09-201-139-14	Sequence 14, Appl1
41	544	71.6	105	4 US-09-120-131-14	Sequence 14, Appl1
42	544	71.6	105	4 US-08-627-610-8	Sequence 8, Appl1
43	533	70.1	130	2 US-08-581-918A-8	Sequence 8, Appl1
44	533	70.1	130	3 US-08-346-147B-8	Sequence 8, Appl1
45	533	70.1	130	4 US-08-346-147B-8	Sequence 8, Appl1

## ALIGNMENTS

RESULT 1  
US-08-154-915-4  
; Sequence 4, Application US/08154915  
; Patent No. 5618669  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David  
; APPLICANT: Xiong, Yue  
; TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses  
; TITLE OF INVENTION: Related Thereto  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US 07/888,178  
; FILING DATE: 19-NOV-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/991,997  
; FILING DATE: 17-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/963,308  
; FILING DATE: 16-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/888,178  
; FILING DATE: 26-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/701,514  
; FILING DATE: 16-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 148 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-154-915-4

Query Match 100.0%; Score 760; DB 1; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.6e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAARGVEEYRALLEVALPNAENSYGRPIQVMMGSAVAELLHGA 60

DB 1 MEPSADWLATAARGVEEYRALLEVALPNAENSYGRPIQVMMGSAVAELLHGA 60

QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDMGRLPYDLAEELGHRDVAR 120

DB 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDMGRLPYDLAEELGHRDVAR 120

QY 121 YLRAAAGGTRGSNHARIDAEGPSDIPD 148

DB 121 YLRAAAGGTRGSNHARIDAEGPSDIPD 148

RESULT 2

US-08-384-106A-16

Sequence 16, Application US/08384106A

Patent No. 6033847

GENERAL INFORMATION:

APPLICANT: Sheer Ph.D., Charles J.

APPLICANT: Downing M.D., James

APPLICANT: Hirai Ph.D., Hiroshi

APPLICANT: Okuda, Tsukasa

TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESSES:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/384,106A

FILING DATE: 06-FEB-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Fox, Samuel L.

REGISTRATION NUMBER: 30,353

REFERENCE/DOCKET NUMBER: 0656, 0500000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 148 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-384-106A-16

Query Match 100.0%; Score 760; DB 3; Length 148;

Best Local Similarity 100.0%; Pred. No. 1.6e-83;

Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAARGVEEYRALLEVALPNAENSYGRPIQVMMGSAVAELLHGA 60

DB 1 MEPSADWLATAARGVEEYRALLEVALPNAENSYGRPIQVMMGSAVAELLHGA 60

QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDMGRLPYDLAEELGHRDVAR 120

DB 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDMGRLPYDLAEELGHRDVAR 120

QY 121 YLRAAAGGTRGSNHARIDAEGPSDIPD 148

DB 121 YLRAAAGGTRGSNHARIDAEGPSDIPD 148

RESULT 3

US-08-384-106A-24

Sequence 24, Application US/08384106A

Patent No. 6033847

GENERAL INFORMATION:

APPLICANT: Sheer Ph.D., Charles J.

APPLICANT: Downing M.D., James

APPLICANT: Hirai Ph.D., Hiroshi

APPLICANT: Okuda, Tsukasa

TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESSES:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/384,106A

FILING DATE: 06-FEB-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Fox, Samuel L.

REGISTRATION NUMBER: 30,353

REFERENCE/DOCKET NUMBER: 0656, 0500000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 148 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-384-106A-24

Query Match 100.0%; Score 760; DB 3; Length 148;

Best Local Similarity 100.0%; Pred. No. 1.6e-83;

Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAARGVEEYRALLEVALPNAENSYGRPIQVMMGSAVAELLHGA 60

DB 1 MEPSADWLATAARGVEEYRALLEVALPNAENSYGRPIQVMMGSAVAELLHGA 60

QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDMGRLPYDLAEELGHRDVAR 120

DB 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDMGRLPYDLAEELGHRDVAR 120

QY 121 YLRAAAGGTRGSNHARIDAEGPSDIPD 148

DB 121 YLRAAAGGTRGSNHARIDAEGPSDIPD 148

RESULT 4



PCT-US93-09945-4  
; Sequence 4, Application PC/TUS9309945  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses Related  
; NUMBER OF SEQUENCES: 4  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/09945  
; FILING DATE:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 07/963,308  
; FILING DATE: 16-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/991,997  
; FILING DATE: 17-DEC-1992  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 148 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US93-09945-4

Query Match 100.0%; Score 760; DB 5; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.6e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEERALLLEAVALPNAFNSYGRPIQVMMGSAFYAEILLHGA 60  
DB 1 MEPSADWLATAAARGVEERALLLEAVALPNAFNSYGRPIQVMMGSAFYAEILLHGA 60

QY 61 EPNCADPATLTRPVHDARREGFLDTLVVLRAGARLDVDRMGRLPVDLAEEELGHRDVAR 120  
DB 61 EPNCADPATLTRPVHDARREGFLDTLVVLRAGARLDVDRMGRLPVDLAEEELGHRDVAR 120

QY 121 YLRAAAGTGRGSHARIDAEGPSDIPD 148  
DB 121 YLRAAAGTGRGSHARIDAEGPSDIPD 148

RESULT 5  
-627-610-2  
; Sequence 2, Application US/08627610  
; Patent No. 5919997  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Delrinho, Ronald A.  
; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/627,610  
; FILING DATE: 04-APR-1996

CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: CSI-001CP6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 156 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-627-610-2

Query Match 100.0%; Score 760; DB 2; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.7e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEERALLLEAVALPNAFNSYGRPIQVMMGSAFYAEILLHGA 60  
DB 9 MEPSADWLATAAARGVEERALLLEAVALPNAFNSYGRPIQVMMGSAFYAEILLHGA 68

QY 61 EPNCADPATLTRPVHDARREGFLDTLVVLRAGARLDVDRMGRLPVDLAEEELGHRDVAR 120  
DB 69 EPNCADPATLTRPVHDARREGFLDTLVVLRAGARLDVDRMGRLPVDLAEEELGHRDVAR 128

QY 121 YLRAAAGTGRGSHARIDAEGPSDIPD 148  
DB 129 YLRAAAGTGRGSHARIDAEGPSDIPD 156

RESULT 6  
US-08-306-511A-2  
; Sequence 2, Application US/08306511A  
; Patent No. 5962316  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannon, Gregory J.  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/306,511A  
; FILING DATE: 14-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: CSI-001CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 156 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-306-511A-2

Query Match 100.0%; Score 760; DB 2; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.7e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALLLEAVLPNAPNSYGRPIQVMMGSAVAEILLHGA 60  
Db 9 MEPSADWLATAAARGVEEVRALLLEAVLPNAPNSYGRPIQVMMGSAVAEILLHGA 68

QY 61 EPNCADPATLTRPVHDAAREGFDTLVVLRAGARLDVDMGRLPVDLAEEIGHRDVAR 120  
Db 69 EPNCADPATLTRPVHDAAREGFDTLVVLRAGARLDVDMGRLPVDLAEEIGHRDVAR 128

QY 121 YLRAAGGTGSGNHARIDAAEGPSDIPD 148  
Db 129 YLRAAGGTGSGNHARIDAAEGPSDIPD 156

RESULT 7  
US-08-893-274-2  
Sequence 2, Application US/08893274  
Patent No. 5968821  
GENERAL INFORMATION:  
APPLICANT: Beach, David H.  
APPLICANT: Demetrick, Douglas J.  
APPLICANT: Serrano, Manuel  
APPLICANT: Hannon, Gregory J.  
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/893,274  
FILING DATE: 15-JULY-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,511  
FILING DATE: 14-SEPTEMBER-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,812  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,371  
FILING DATE: 14-APRIL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/154,915  
FILING DATE: 18-NOVEMBER-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/991,997  
FILING DATE: 17-DECEMBER-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/963,308  
FILING DATE: 16-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-071.09  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1000

TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-893-274-2

Query Match 100.0%; Score 760; DB 2; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.7e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALLLEAVLPNAPNSYGRPIQVMMGSAVAEILLHGA 60  
Db 9 MEPSADWLATAAARGVEEVRALLLEAVLPNAPNSYGRPIQVMMGSAVAEILLHGA 68

QY 61 EPNCADPATLTRPVHDAAREGFDTLVVLRAGARLDVDMGRLPVDLAEEIGHRDVAR 120  
Db 69 EPNCADPATLTRPVHDAAREGFDTLVVLRAGARLDVDMGRLPVDLAEEIGHRDVAR 128

QY 121 YLRAAGGTGSGNHARIDAAEGPSDIPD 148  
Db 129 YLRAAGGTGSGNHARIDAAEGPSDIPD 156

RESULT 8  
US-08-581-918A-2  
Sequence 2, Application US/08581918A  
Patent No. 6043030  
GENERAL INFORMATION:  
APPLICANT: Beach, David H.  
APPLICANT: Demetrick, Douglas J.  
APPLICANT: Serrano, Manuel  
APPLICANT: Hannon, Gregory J.  
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley, Hoag & Elliot  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordpad  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/581,918A  
FILING DATE: 02-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/497,214  
FILING DATE: 30-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/346,147  
FILING DATE: 29-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,511  
FILING DATE: 14-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,812  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,371  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/154,915  
FILING DATE: 18-NOV-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/991,997  
FILING DATE: 17-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-071.06  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1299  
TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-581-918A-2

Query Match 100.0%; Score 760; DB 3; Length 156;  
Local Similarity 100.0%; Pred. No. 1,7e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSADWLATAARGVEEVRALLEAVALPNASVGRPIQVMMGSAVAELLILHGA 60  
DB 9 MESSADWLATAARGVEEVRALLEAVALPNASVGRPIQVMMGSAVAELLILHGA 68  
QY 61 EPNCADPATLTTPVHDAREGFLDTLVLRAGARLDVDAWGRLPVDLAEELGHRDVAR 120  
DB 69 EPNCADPATLTTPVHDAREGFLDTLVLRAGARLDVDAWGRLPVDLAEELGHRDVAR 128  
QY 121 YLRAAGGTRGSNHARIDAEGPSDIPD 148  
DB 129 YLRAAGGTRGSNHARIDAEGPSDIPD 156

RESULT 9

US-08-346-147B-2  
Sequence 2, Application US/08346147B  
Patent No. 6211334  
GENERAL INFORMATION:  
APPLICANT: Beach, David H.  
APPLICANT: Demetrick, Douglas J.  
APPLICANT: Serrano, Manuel  
APPLICANT: Hannon, Gregory J.  
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
TITLE OF INVENTION: Related Thereto  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley, Hoag & Eliot  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPad  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/346,147B  
FILING DATE: 29-NOV-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,511  
FILING DATE: 14-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,812  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,371  
FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/154,915  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/991,997  
FILING DATE: 17-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-071.04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1299  
TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-346-147B-2

Query Match 100.0%; Score 760; DB 4; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1,7e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSADWLATAARGVEEVRALLEAVALPNASVGRPIQVMMGSAVAELLILHGA 60  
DB 9 MESSADWLATAARGVEEVRALLEAVALPNASVGRPIQVMMGSAVAELLILHGA 68  
QY 61 EPNCADPATLTTPVHDAREGFLDTLVLRAGARLDVDAWGRLPVDLAEELGHRDVAR 120  
DB 69 EPNCADPATLTTPVHDAREGFLDTLVLRAGARLDVDAWGRLPVDLAEELGHRDVAR 128  
QY 121 YLRAAGGTRGSNHARIDAEGPSDIPD 148  
DB 129 YLRAAGGTRGSNHARIDAEGPSDIPD 156

RESULT 10

US-08-822-936-2  
Sequence 2, Application US/08822936  
Patent No. 6242575  
GENERAL INFORMATION:  
APPLICANT: Massague, Joan  
APPLICANT: Roberts, James M.  
APPLICANT: Koff, Andrew  
APPLICANT: Polyak, Kornelia  
TITLE OF INVENTION: Isolated p27 Protein, Nucleic Acid  
TITLE OF INVENTION: Molecules Encoding Same, Methods of Identifying Agents Acti  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley, Hoag & Eliot, LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/822,936  
FILING DATE: 21-FEBRUARY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-079.05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1000

RESULT 13  
US-08-474-177-2  
; Sequence 2, Application US/08474177  
; Patent No. 5624819

GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,177  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-177-2

Query Match 99.1%; Score 753; DB 1; Length 156;  
Best Local Similarity 99.3%; Pred. No. 1.2e-82;  
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPSADMLATAAARGVEEVRALLEAVLPNAPNSYGRPIQVMMGASARVAEILLHGA 60  
DB 9 MEPSADMLATAAARGVEEVRALLEAGALPNAPNSYGRPIQVMMGASARVAEILLHGA 68  
QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRAMGRLLPVDLAEEELGHRDVAR 120  
DB 69 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRAMGRLLPVDLAEEELGHRDVAR 128  
QY 121 YLRAAAGTGRGSHARIDAEGPSDIPD 148  
DB 129 YLRAAAGTGRGSHARIDAEGPSDIPD 156

RESULT 14  
US-08-487-033-2  
Sequence 2, Application US/08487033  
Patent No. 5739027  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1-Beta GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,033  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-487-033-2

Query Match 99.1%; Score 753; DB 1; Length 156;  
Best Local Similarity 99.3%; Pred. No. 1.2e-82;  
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPSADMLATAAARGVEEVRALLEAVLPNAPNSYGRPIQVMMGASARVAEILLHGA 60  
DB 9 MEPSADMLATAAARGVEEVRALLEAGALPNAPNSYGRPIQVMMGASARVAEILLHGA 68  
QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRAMGRLLPVDLAEEELGHRDVAR 120  
DB 69 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRAMGRLLPVDLAEEELGHRDVAR 128  
QY 121 YLRAAAGTGRGSHARIDAEGPSDIPD 148  
DB 129 YLRAAAGTGRGSHARIDAEGPSDIPD 156

RESULT 15

US-08-480-810-2

; Sequence 2, Application US/08480810

; Patent No. 5801236

; GENERAL INFORMATION:

; APPLICANT: Kamb, Alexander

; TITLE OF INVENTION: MTS1 GENE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Venable, Baetjer, Howard &amp; Civiletti, LLP

; STREET: 1201 New York Avenue, Suite 1000

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/480,810

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/03316

; FILING DATE: 17-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/251,938

; FILING DATE: 01-JUN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/215,087

; FILING DATE: 18-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/215,086

; FILING DATE: 18-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/214,582

; FILING DATE: 18-MAR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Innen, Jeffrey L.

; REGISTRATION NUMBER: 28,957

; REFERENCE/DOCKET NUMBER: 24884-109348

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-962-4810

; TELEFAX: 202-962-8300

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 156 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-480-810-2

Query Match 99.1%; Score 753; DB 1; Length 156;  
Best Local Similarity 99.3%; Pred No. 1.2e-82;  
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MEPSADWLATAAARGVEEVRALLLEAVALLPNAIPNSYGRPIQVMMGSAFYAEILLHGA 60
DB 9 MEPSADWLATAAARGVEEVRALLLEAGALLPNAIPNSYGRPIQVMMGSAFYAEILLHGA 68
OY 61 EPNCADPRLTLRPVVDARREGFLDTLVVLRAGARLDVDAWGRLPVDLAEEELGHRDVAR 120
DB 69 EPNCADPRLTLRPVVDARREGFLDTLVVLRAGARLDVDAWGRLPVDLAEEELGHRDVAR 128
OY 121 YLRAAAGTGRGSHARIDAABGSPDIPD 148
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DB 129 YLRAAAGTGRGSHARIDAABGSPDIPD 156

Search completed: September 19, 2002, 17:24:00  
Job time: 58 sec

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: September 19, 2002, 17:25:12 ; Search time 12.89 Seconds  
(without alignments)  
280.449 Million cell updates/sec

Title: US-09-016-869b-35  
Perfect score: 148  
Sequence: 1 MEPSADWLATAARGRVEV.....TRGSNHARIDAEGSPDIPD 148

Scoring table: OLIGO  
Gapop 60.0 , Gapept 60.0

Searched: 231628 seqs, 24425594 residues

Size: 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

## Database :

1: Issued\_Patents\_AA:\*  
2: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
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4: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	148	100.0	148	1 US-08-154-915-4	Sequence 4, Appl
2	148	100.0	148	3 US-08-384-106A-16	Sequence 16, Appl
3	148	100.0	148	3 US-08-384-106A-24	Sequence 24, Appl
4	148	100.0	148	5 PCT-US93-09945-4	Sequence 4, Appl
5	148	100.0	156	2 US-08-627-610-2	Sequence 2, Appl
6	148	100.0	156	2 US-08-306-511A-2	Sequence 2, Appl
7	148	100.0	156	2 US-08-893-274-2	Sequence 2, Appl
8	148	100.0	156	3 US-08-581-918A-2	Sequence 2, Appl
9	148	100.0	156	4 US-08-346-147B-2	Sequence 2, Appl
10	148	100.0	156	4 US-08-822-936-2	Sequence 2, Appl
11	148	100.0	156	5 PCT-US95-04636-2	Sequence 2, Appl
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13	148	100.0	156	1 US-08-474-177-2	Sequence 2, Appl
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16	148	100.0	156	2 US-08-508-735-2	Sequence 2, Appl
17	148	100.0	156	2 US-08-848-251-2	Sequence 2, Appl
18	148	100.0	156	3 US-08-486-047-2	Sequence 2, Appl
19	148	100.0	156	3 US-09-120-130-2	Sequence 2, Appl
20	148	100.0	156	3 US-09-115-252-2	Sequence 2, Appl
21	148	100.0	156	3 US-08-986-515-2	Sequence 2, Appl
22	148	100.0	156	4 US-09-120-128-2	Sequence 2, Appl
23	148	100.0	156	4 US-09-120-129-2	Sequence 2, Appl
24	148	100.0	156	4 US-09-201-139-2	Sequence 2, Appl
25	148	100.0	156	4 US-09-120-131-2	Sequence 2, Appl
26	148	100.0	156	4 US-08-910-722-2	Sequence 2, Appl
27	148	100.0	105	1 US-08-474-177-14	Sequence 14, Appl

28	105	70.9	105	1 US-08-487-033-14	Sequence 14, Appl
29	105	70.9	105	1 US-08-480-810-14	Sequence 14, Appl
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43	72	48.6	88	3 US-08-581-918A-38	Sequence 38, Appl
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46	72	48.6	137	5 US-08-306-511A-4	Sequence 4, Appl
47	72	48.6	137	2 US-08-893-274-4	Sequence 4, Appl
48	72	48.6	138	1 US-08-474-177-16	Sequence 16, Appl
49	72	48.6	138	1 US-08-487-033-16	Sequence 16, Appl
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51	72	48.6	138	2 US-08-508-735-16	Sequence 16, Appl
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54	72	48.6	138	2 US-08-486-047-16	Sequence 16, Appl
55	72	48.6	138	3 US-08-384-106A-25	Sequence 25, Appl
56	72	48.6	138	3 US-09-120-130-16	Sequence 16, Appl
57	72	48.6	138	3 US-08-581-918A-4	Sequence 16, Appl
58	72	48.6	138	3 US-09-115-252-16	Sequence 16, Appl
59	72	48.6	138	3 US-08-986-515-16	Sequence 16, Appl
60	72	48.6	138	4 US-09-120-128-16	Sequence 16, Appl
61	72	48.6	138	4 US-09-120-129-16	Sequence 16, Appl
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65	72	48.6	138	4 US-08-822-936-4	Sequence 4, Appl
66	72	48.6	138	5 PCT-US95-04636-4	Sequence 4, Appl
67	62	41.9	77	2 US-08-893-274-8	Sequence 8, Appl
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69	62	41.9	130	2 US-08-627-610-8	Sequence 8, Appl
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71	62	41.9	130	4 US-08-346-147B-8	Sequence 8, Appl
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73	62	41.9	130	5 PCT-US95-04636-8	Sequence 8, Appl
74	52	35.1	52	1 US-08-249-371-2	Sequence 2, Appl
75	52	35.1	52	5 PCT-US95-06451-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-154-915-4  
; Sequence 4, Application US/08154915  
; Patent No. 5618669  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David  
; TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses  
; TITLE OF INVENTION: Related Thereto  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/154, 915
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIT-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-154-915-4

Query Match          100.0%; Score 148; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 1,4e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESPADWLTAARGVEEVALLEAVLPNAPNSYGRRIQVMMGSAVAELLHLGA 60
    |||||||
DB 1 MESPADWLTAARGVEEVALLEAVLPNAPNSYGRRIQVMMGSAVAELLHLGA 60
    |||||||

QY 61 EPNCADPATLTRPVHDAREGEFLDTLVYLHRAGARLDVRDAGRLPYDLAEELGHRDVAR 120
    |||||||
DB 61 EPNCADPATLTRPVHDAREGEFLDTLVYLHRAGARLDVRDAGRLPYDLAEELGHRDVAR 120
    |||||||

QY 121 YLRAAGGTGSGNHARIDAAEGPSDIPD 148
    |||||||
DB 121 YLRAAGGTGSGNHARIDAAEGPSDIPD 148
    |||||||

RESULT 2
US-08-384-106A-16
; Sequence 16, Application US/08384106A
; Patent No. 6033847
; GENERAL INFORMATION:
; APPLICANT: Sherr Ph.D., Charles J.
; APPLICANT: Downing M.D., James
; APPLICANT: Hirai Ph.D., Hiroshi
; APPLICANT: Okuda, Tsukasa
; TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of
; CYCLE OF INVENTION: Cyclin dependent kinases CDK4 and CDK6, and Uses Thereof
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/384,106A
; FILING DATE: 06-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0500000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-384-106A-16

Query Match          100.0%; Score 148; DB 3; Length 148;
Best Local Similarity 100.0%; Pred. No. 1,4e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESPADWLTAARGVEEVALLEAVLPNAPNSYGRRIQVMMGSAVAELLHLGA 60
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DB 1 MESPADWLTAARGVEEVALLEAVLPNAPNSYGRRIQVMMGSAVAELLHLGA 60
    |||||||

QY 61 EPNCADPATLTRPVHDAREGEFLDTLVYLHRAGARLDVRDAGRLPYDLAEELGHRDVAR 120
    |||||||
DB 61 EPNCADPATLTRPVHDAREGEFLDTLVYLHRAGARLDVRDAGRLPYDLAEELGHRDVAR 120
    |||||||

QY 121 YLRAAGGTGSGNHARIDAAEGPSDIPD 148
    |||||||
DB 121 YLRAAGGTGSGNHARIDAAEGPSDIPD 148
    |||||||

RESULT 3
US-08-384-106A-24
; Sequence 24, Application US/08384106A
; Patent No. 6033847
; GENERAL INFORMATION:
; APPLICANT: Sherr Ph.D., Charles J.
; APPLICANT: Downing M.D., James
; APPLICANT: Hirai Ph.D., Hiroshi
; APPLICANT: Okuda, Tsukasa
; TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of
; CYCLE OF INVENTION: Cyclin dependent kinases CDK4 and CDK6, and Uses Thereof
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/384,106A
; FILING DATE: 06-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0500000
; TELECOMMUNICATION INFORMATION:
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TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 24  
SEQUENCE CHARACTERISTICS:  
LENGTH: 148 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-384-1066-24

Query Match	100.0%;	Score 148;	DB 3;	Length 148;
Best Local Similarity	100.0%;	Pred. No. 1.4e-130;		
Matches 148; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy	Db	Qy	Db
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MEPSADMTATAAGRGVEEVALLLEAAALPAPASYSRPTIQVMMGMSAVAEITLLHGA	MEPSADMTATAAGRGVEEVALLLEAAALPAPASYSRPTIQVMMGMSAVAEITLLHGA	60	60
1	1	1	1
MEPSADMTATAAGRGVEEVALLLEAAALPAPASYSRPTIQVMMGMSAVAEITLLHGA	MEPSADMTATAAGRGVEEVALLLEAAALPAPASYSRPTIQVMMGMSAVAEITLLHGA	60	60
61	61	61	61
EPNCADPPTLTLPVHDARREGFDLTLYVHHAGARLDVPMAGSLPVDLAELGHRDVAR	EPNCADPPTLTLPVHDARREGFDLTLYVHHAGARLDVPMAGSLPVDLAELGHRDVAR	120	120
61	61	61	61
EPNCADPPTLTLPVHDARREGFDLTLYVHHAGARLDVPMAGSLPVDLAELGHRDVAR	EPNCADPPTLTLPVHDARREGFDLTLYVHHAGARLDVPMAGSLPVDLAELGHRDVAR	120	120
121	121	121	121
YLRAAAGGTGCSNNARIDAAEPSPDIPD	YLRAAAGGTGCSNNARIDAAEPSPDIPD	148	148
121	121	121	121
YLRAAAGGTGCSNNARIDAAEPSPDIPD	YLRAAAGGTGCSNNARIDAAEPSPDIPD	148	148

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RESULT      4
PCT-US93-09945-4
; Sequence 4, Application PC/TUS9309945
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses Related
; TITLE OF INVENTION: There to
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09945
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
PCT-US93-09945-4

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Query Match	100.0%	Score 148;	DB 5;	Length 148;
Best Local Similarity	100.0%	Pred. No. 1.4e-130;		
Matches 148; Conservative	0;	Mismatches	0;	Gaps 0;

Qy	1	MEPSADMLTAAARCRVEEVRALLLEAVALLPNAAPNSYGRPLQVMMKMSARVAELLILLHGA	60
Db	1	MEPSADMLTAAARCRVEEVRALLLEAVALLPNAAPNSYGRPLQVMMKMSARVAELLILLHGA	60
Qy	61	EPNCADPATLTLPVHDAAKEGFLPTLVYLHRRAGARLDV RDAMGRLPYDLAEELGHRVAR	120
Db	61	EPNCADPATLTLPVHDAAKEGFLPTLVYLHRRAGARLDV RDAMGRLPYDLAEELGHRVAR	120
Qy	121	YLFNAAGGTGRGSNHARIDAAEESPDPD	148

Db 121 YLRAAGTSGSNHARIDAAEGPSDIPD 148

RESULT 5  
US-08-627-610-2

; Sequence 2, Application US/08627610  
; Patent No. 5919997

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1  GENERAL INFORMATION:
2
3  APPLICANT: Beach, David H.
4
5  APPLICANT: Serrano, Manuel
6
7  APPLICANT: Deflino, Ronald A.
8
9  TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
10
11 TITLE OF INVENTION: Regulation
12
13 NUMBER OF SEQUENCES: 13
14
15 CORRESPONDENCE ADDRESS:
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```

```

1 ADDRESS: LAHIVE & COCKFIELD
2 STREET: 60 State Street
3 CITY: Boston
4 STATE: MA
5 COUNTRY: USA
6 ZIP: 02109
7
8 COMPUTER READABLE FORM:
9
10 MEDIUM TYPE: Floppy disk
11 COMPUTER: IBM PC compatible
12 OPERATING SYSTEM: PC-DOS/MS-DOS
13 SOFTWARE: ASCII(text)
14
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/627,610
17 FILING DATE: 04-APR-1996
18
19 CLASSIFICATION: 800
20
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Vincent, Matthew P.
23 REGISTRATION NUMBER: 36,709
24 REFERENCE/DOCKET NUMBER: CSI-001CP6
25
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (617) 227-7400
28 TELEFAX: (617) 227-5941
29
30 INFORMATION FOR SEO ID NO: 2:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 156 amino acids
33 TYPE: amino acid
34
35 TOPOLOGY: linear
36
37 MOLECULE TYPE: protein
38
39 US-08-627-610-2

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Query Match	100.0%;	Score 148;	DB 2;	Length 156;
Best Local Similarity	100.0%;	Pred. No. 1.5e130;		
Matches 148;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

QY	1	MESASAWLATAAARGVEVEVRLTAEVALLPNAPNSYGRPIQVMMGSAKVAEELLTHGA	60
QY	9	MESASAWLATAAARGVEVEVRLTAEVALLPNAPNSYGRPIQVMMGSAKVAEELLTHGA	68
Db			
QY	61	EPNCADPATLTRVPHDAAEGLDPLVYLHRGALDYRDAMGRPLVDIAEEGHRVAR	120
QY	69	EPNCADPATLTRVPHDAAEGLDPLVYLHRGALDYRDAMGRPLVDIAEEGHRVAR	128
Db			
QY	121	YLRAAAGTGRGSNHARIDAEGSPDIPD	148
QY	129	YLRAAAGTGRGSNHARIDAEGSPDIPD	156
Db			

## RESULT 6

US-08-306-511A-2  
; Sequence 2, Application US/08306511A  
; Patent No. 5962316

GENERAL INFORMATION:  
APPLICANT: Beach, David H.  
APPLICANT: Demetrick, Douglas J.  
APPLICANT: Serrano, Manuel  
APPLICANT: Hannon, Gregory J.

```

; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,511A
; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-306-511A-2

Query Match      100.0%; Score 148; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAARGVEEVRALLLEAVLPNAPNSYGRPIQVMMGSAVAVELLHLHGA 60
    |||||||
DB 9 MEPSADWLATAARGVEEVRALLLEAVLPNAPNSYGRPIQVMMGSAVAVELLHLHGA 68
QY 61 EPNCADPATLTRPVHDAAREGFIDTLVYLHRAAGARLDVDMGRLPVDLAELGHRDVAR 120
    |||||||
DB 69 EPNCADPATLTRPVHDAAREGFIDTLVYLHRAAGARLDVDMGRLPVDLAELGHRDVAR 128
QY 121 YLRAAAGGTRGSNHARIDAEGPSDIPD 148
    |||||||
    129 YLRAAAGGTRGSNHARIDAEGPSDIPD 156

RESULT 7
; US-08-893-274-2
; Sequence 2, Application US/08893274
; Patent No. 5968821
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
; TITLE OF INVENTION: and Uses Related Thereto
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,274
; FILING DATE: 15-JULY-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APRIL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOVEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DECEMBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-893-274-2

Query Match      100.0%; Score 148; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAARGVEEVRALLLEAVLPNAPNSYGRPIQVMMGSAVAVELLHLHGA 60
    |||||||
DB 9 MEPSADWLATAARGVEEVRALLLEAVLPNAPNSYGRPIQVMMGSAVAVELLHLHGA 68
QY 61 EPNCADPATLTRPVHDAAREGFIDTLVYLHRAAGARLDVDMGRLPVDLAELGHRDVAR 120
    |||||||
DB 69 EPNCADPATLTRPVHDAAREGFIDTLVYLHRAAGARLDVDMGRLPVDLAELGHRDVAR 128
QY 121 YLRAAAGGTRGSNHARIDAEGPSDIPD 148
    |||||||
    129 YLRAAAGGTRGSNHARIDAEGPSDIPD 156

RESULT 8
; US-08-581-918A-2
; Sequence 2, Application US/08581918A
; Patent No. 6043030
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT
; STREET: One Post Office Square
; CITY: Boston
```

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STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-581-918A-2

Query Match          100.0%; Score 148; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 MPPSADWLATAAARGVEEVRALLLEAVLPNAPNSYGRPTQVMMGSAFYAEILLHGA 60
9 MPPSADWLATAAARGVEEVRALLLEAVLPNAPNSYGRPTQVMMGSAFYAEILLHGA 68
61 EPNCADPATLTTPVHDARREGFLDTLVVLRAGARLDVDRDAMGRPLPYDLAEELGHRDVAR 120
69 EPNCADPATLTTPVHDARREGFLDTLVVLRAGARLDVDRDAMGRPLPYDLAEELGHRDVAR 128
121 YLRAAAGGTGSGNHARIDAEGPSDIPD 148
129 YLRAAAGGTGSGNHARIDAEGPSDIPD 156

RESULT 9
US-08-346-147B-2
; Sequence 2, Application US/08346147B
; Patent No. 6211334
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
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```
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,147B
FILING DATE: 29-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-346-147B-2

Query Match          100.0%; Score 148; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 MPPSADWLATAAARGVEEVRALLLEAVLPNAPNSYGRPTQVMMGSAFYAEILLHGA 60
9 MPPSADWLATAAARGVEEVRALLLEAVLPNAPNSYGRPTQVMMGSAFYAEILLHGA 68
61 EPNCADPATLTTPVHDARREGFLDTLVVLRAGARLDVDRDAMGRPLPYDLAEELGHRDVAR 120
69 EPNCADPATLTTPVHDARREGFLDTLVVLRAGARLDVDRDAMGRPLPYDLAEELGHRDVAR 128
121 YLRAAAGGTGSGNHARIDAEGPSDIPD 148
129 YLRAAAGGTGSGNHARIDAEGPSDIPD 156

RESULT 10
US-08-822-936-2
; Sequence 2, Application US/08822936
; Patent No. 6242575
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INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 391 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-589-981-2

Query Match 100.0%; Score 148; DB 1; Length 391;  
Best Local Similarity 100.0%; Pred. No. 3.5e-130;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPADMTATTAARGREYVALLLEVALPAPNSYGRPIQVMMGSARVAEELLHGA 60  
DB 244 MEPADMTATTAARGREYVALLLEVALPAPNSYGRPIQVMMGSARVAEELLHGA 303  
QY 61 EPNCADPATLTRPYHDARREGFLDTLVLRHAGARLDVPRAMGRPLVDLAEEIGHRDVAR 120  
DB 304 EPNCADPATLTRPYHDARREGFLDTLVLRHAGARLDVPRAMGRPLVDLAEEIGHRDVAR 363  
QY 121 YLRAAGTGRGSHNRARIDAAEGPSDIPD 148  
DB 364 YLRAAGTGRGSHNRARIDAAEGPSDIPD 391

RESULT 13  
US-08-474-177-2

Sequence 2, Application US/08474177  
Patent No. 5624819  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
TITLE OF INVENTION: GERM LINE MUTATIONS IN THE MTS GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,177  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348-E

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-177-2

Query Match 81.8%; Score 121; DB 1; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2.1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSARVAEELLHGAEPNCADPATLTRPYHDAREGFLDTLV 87  
DB 36 ALPNAPNSYGRPIQVMMGSARVAEELLHGAEPNCADPATLTRPYHDAREGFLDTLV 95  
QY 88 VLHAGARLDVPRAMGRPLVDLAEEIGHRDVARYLRAAGTGRGSHNRARIDAAEGPSDIP 147  
DB 96 VLHAGARLDVPRAMGRPLVDLAEEIGHRDVARYLRAAGTGRGSHNRARIDAAEGPSDIP 155  
QY 148 D 148  
DB 156 D 156

RESULT 14

US-08-487-033-2

Sequence 2, Application US/08487033  
Patent No. 5739027  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1E1-Beta GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,033  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-487-033-2

Query Match 81.8%; Score 121; DB 1; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2,1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

28 ALPNAPNSYGRPIQVMMGSAVAVELLHGAEPNCADPATLTRPVHDAREGFLDTLV 87  
|||||  
36 ALPNAPNSYGRPIQVMMGSAVAVELLHGAEPNCADPATLTRPVHDAREGFLDTLV 95  
|||||  
QY 88 VLHAGARLDVWDAGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPSDIP 147  
|||||  
DB 96 VLHAGARLDVWDAGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPSDIP 155  
|||||  
QY 148 D 148  
DB 156 D 156

RESULT 15  
US-08-480-810-2  
Sequence 2, Application US/08480810  
Patent No. 5801236  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,810  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-480-810-2

Query Match 81.8%; Score 121; DB 1; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2,1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAVAVELLHGAEPNCADPATLTRPVHDAREGFLDTLV 87  
|||||  
DB 36 ALPNAPNSYGRPIQVMMGSAVAVELLHGAEPNCADPATLTRPVHDAREGFLDTLV 95  
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QY 88 VLHAGARLDVWDAGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPSDIP 147  
|||||  
DB 96 VLHAGARLDVWDAGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPSDIP 155  
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QY 148 D 148  
DB 156 D 156

RESULT 16  
US-08-508-735-2  
Sequence 2, Application US/08508735  
Patent No. 5843756  
GENERAL INFORMATION:  
APPLICANT: Stone, Steven  
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/508,735  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: US to be assigned  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4848  
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-508-735-2

Query Match 81.8%; Score 121; DB 2; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2,1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAVAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87  
DB 36 ALPNAPNSYGRPIQVMMGSAVAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 95

QY 88 VLRAGARLDVDRAMGRPLPVDLAEEIGHRDVARYLRAAAGTGRSNNARIDAAGSPDIP 147  
DB 96 VLRAGARLDVDRAMGRPLPVDLAEEIGHRDVARYLRAAAGTGRSNNARIDAAGSPDIP 155

QY 148 D 148  
DB 156 D 156

RESULT 17  
US-08-848-251-2  
Sequence 2, Application US/0848251  
Patent No. 5989815  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND  
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS  
TITLE OF INVENTION: GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/848,251  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/474,083  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-848-251-2

Query Match 81.8%; Score 121; DB 2; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2,1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAVAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87  
DB 36 ALPNAPNSYGRPIQVMMGSAVAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 95

QY 88 VLRAGARLDVDRAMGRPLPVDLAEEIGHRDVARYLRAAAGTGRSNNARIDAAGSPDIP 147  
DB 96 VLRAGARLDVDRAMGRPLPVDLAEEIGHRDVARYLRAAAGTGRSNNARIDAAGSPDIP 155

QY 148 D 148  
DB 156 D 156

RESULT 18  
US-08-486-047-2  
Sequence 2, Application US/08486047  
Patent No. 5994095  
GENERAL INFORMATION:  
APPLICANT: Ramb, Alexander  
TITLE OF INVENTION: MTS2 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,047  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-486-047-2

Query Match 81.8%; Score 121; DB 2; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2.1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAKVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87  
DB 36 ALPNAPNSYGRPIQVMMGSAKVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 95  
QY 88 VLHRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 147  
DB 96 VLHRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 155  
QY 148 D 148  
DB 156 D 156

RESULT 19  
US-09-120-130-2  
Sequence 2, Application US/09120130  
Patent No. 6037462  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/120,130  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/480,810  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-120-130-2

Query Match 81.8%; Score 121; DB 3; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2.1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAKVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87  
DB 36 ALPNAPNSYGRPIQVMMGSAKVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 95  
QY 88 VLHRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 147  
DB 96 VLHRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 155  
QY 148 D 148  
DB 156 D 156

RESULT 20  
US-09-115-252-2  
Sequence 2, Application US/09115252  
Patent No. 6060301  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/115,252  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,810  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994



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1      APPLICATION NUMBER:  US 08/215,087
2      FILING DATE:  18-MAR-1994
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER:  US 08/215,086
5      FILING DATE:  18-MAR-1994
6      PRIOR APPLICATION DATA:
7      APPLICATION NUMBER:  US 08/227,369
8      FILING DATE:  14-APR-1994
9      PRIOR APPLICATION DATA:
10     APPLICATION NUMBER:  US 08/214,582
11     FILING DATE:  18-MAR-1994
12     ATTORNEY/AGENT INFORMATION:
13     NAME:  Ihnen, Jeffrey L.
14     REGISTRATION NUMBER:  28,957
15     REFERENCE/DOCKET NUMBER:  24884-109348
16     TELECOMMUNICATION INFORMATION:
17     TELEPHONE:  202-962-4810
18     TELEFAX:  202-962-8300
19     INFORMATION FOR SEQ ID NO:  2:
20     SEQUENCE CHARACTERISTICS:
21     LENGTH: 156 amino acids
22     TYPE: amino acid
23     TOPOLOGY: linear
24     MOLECULE TYPE: protein
25     OS-08-986-515-2

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Query Match	81.8%;	Score 121;	DB 3;	Length 156;
Best Local Similarity	100.0%;	Pred. No. 2.1e-105;		
Matches 121;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

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1      RESULT 22
2      US-09-120-128-2
3      ; Sequence 2, Application US/09120128
4      ; Patent No. 6140473
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Kamb, Alexander
7      ; TITLE OF INVENTION: MTS2 GENE
8      ; NUMBER OF SEQUENCES: 36
9      ; CORRESPONDENCE ADDRESS:
10     ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
11     ; STREET: 1201 New York Avenue, Suite 1000
12     ; CITY: Washington
13     ; STATE: DC
14     ; COUNTRY: USA
15     ; ZIP: 20005
16     ;
17     ; COMPUTER READABLE FORM:
18     ; MEDIUM TYPE: Floppy disk
19     ; COMPUTER: IBM PC compatible
20     ; OPERATING SYSTEM: PC-DOS/MS-DOS
21     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
22     ; CURRENT APPLICATION DATA:
23     ; APPLICATION NUMBER: US/09/120,128
24     ;
25     ; FILING DATE:
26     ; CLASSIFICATION:
27     ; PRIOR APPLICATION DATA:
28     ; APPLICATION NUMBER: US/08/486,047
29     ; FILING DATE: 07-JUN-1995
30     ; APPLICATION NUMBER: PCT/US95/03316
31     ; FILING DATE: 17-MAR-1995
32     ;

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-120-128-2

Query Match      81.8%; Score 121; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.1e-105;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 ALPNAPNSYGRPIQVMMGSAVAELLLHGAEPNCADPATLTRPVHDAREGFLDTLV 87
DB 36 ALPNAPNSYGRPIQVMMGSAVAELLLHGAEPNCADPATLTRPVHDAREGFLDTLV 95
OY 88 VLHRAGARLDVNDAMGRPLVVDLAELGHRDVARYLRAAGSTRGSNHARIDAAEGPSDIP 147
DB 96 VLHRAGARLDVNDAMGRPLVVDLAELGHRDVARYLRAAGSTRGSNHARIDAAEGPSDIP 155
OY 148 D 148
DB 156 D 156

LT 23
9-120-129-2
; Sequence 2, Application US/09120129
; Patent No. 6180776
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,129
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/486,047
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-120-129-2

Query Match      81.8%; Score 121; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.1e-105;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 ALPNAPNSYGRPIQVMMGSAVAELLLHGAEPNCADPATLTRPVHDAREGFLDTLV 87
DB 36 ALPNAPNSYGRPIQVMMGSAVAELLLHGAEPNCADPATLTRPVHDAREGFLDTLV 95
OY 88 VLHRAGARLDVNDAMGRPLVVDLAELGHRDVARYLRAAGSTRGSNHARIDAAEGPSDIP 147
DB 96 VLHRAGARLDVNDAMGRPLVVDLAELGHRDVARYLRAAGSTRGSNHARIDAAEGPSDIP 155
OY 148 D 148
DB 156 D 156

RESULT 24
US-09-201-139-2
; Sequence 2, Application US/09201139
; Patent No. 6210949
; GENERAL INFORMATION:
; APPLICANT: Stone, Steven
; APPLICANT: Jiang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/201,139  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/508,735  
FILING DATE:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4848  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-201-139-2

Query Match 81.8%; Score 121; DB 4; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2.1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAVAELLHLHGAEPNCADPATLTFRPVHDAAREGFLDTLV 87  
DB 36 ALPNAPNSYGRPIQVMMGSAVAELLHLHGAEPNCADPATLTFRPVHDAAREGFLDTLV 95  
QY 88 VLRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 147  
DB 96 VLRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 155  
QY 148 D 148  
DB 156 D 156

RESULT 25  
US-09-120-131-2  
Sequence 2, Application US/09120131  
Patent No. 6218146  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS2 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/120,131  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/486,047  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-120-131-2

Query Match 81.8%; Score 121; DB 4; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2.1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAVAELLHLHGAEPNCADPATLTFRPVHDAAREGFLDTLV 87  
DB 36 ALPNAPNSYGRPIQVMMGSAVAELLHLHGAEPNCADPATLTFRPVHDAAREGFLDTLV 95  
QY 88 VLRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 147  
DB 96 VLRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 155  
QY 148 D 148  
DB 156 D 156

RESULT 26  
US-08-910-722-2  
Sequence 2, Application US/08910722  
Patent No. 6251871  
GENERAL INFORMATION:  
APPLICANT: Jin, Xiaomei  
TITLE OF INVENTION: P16 EXPRESSION CONSTRUCTS AND THEIR  
APPLICATION IN CANCER THERAPY  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,722  
FILING DATE:

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/502,881
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: INGN:016/HYL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
08-910-722-2
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Query Match      81.8%; Score 121; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.1e-105;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 28 ALPNAPNSYGRPIQVMMGSAFYAEILLHGAEPCADPATLTRPYHDAREGFLDTLV 87
Db 36 ALPNAPNSYGRPIQVMMGSAFYAEILLHGAEPCADPATLTRPYHDAREGFLDTLV 95
QY 88 VLHRAGARLDVDRAMGRLPVDLAELGHRDVARYLRAAAGSTRGSNHARIDAAEGPSDIP 147
Db 96 VLHRAGARLDVDRAMGRLPVDLAELGHRDVARYLRAAAGSTRGSNHARIDAAEGPSDIP 155
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QY 148 D 148
Db 156 D 156
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RESULT 27
US-08-474-177-14
Sequence 14, Application US/08474177
Patent No. 5624819
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
```

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FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-177-14
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Query Match      70.9%; Score 105; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-90;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 44 MMGSAFYAEILLHGAEPCADPATLTRPYHDAREGFLDTLVVHLHRAGARLDVDRAMG 103
Db 1 MMGSAFYAEILLHGAEPCADPATLTRPYHDAREGFLDTLVVHLHRAGARLDVDRAMG 60
QY 104 RLPLDLAEELGHRDVARYLRAAAGSTRGSNHARIDAAEGPSDIP 148
Db 61 RLPLDLAEELGHRDVARYLRAAAGSTRGSNHARIDAAEGPSDIP 105
```

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RESULT 28
US-08-487-033-14
Sequence 14, Application US/08487033
Patent No. 5739027
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1-Beta GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-487-033-14

Query Match 70.9%; Score 105; DB 1: Length 105;  
Best Local Similarity 100.0%; Pred. No. 1,1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSARVAEELLHGAEPCADPATLTRPVHDAREGFDLTVLHRRAGARLDVVDAMG 103  
|||||  
DB 1 MMGSARVAEELLHGAEPCADPATLTRPVHDAREGFDLTVLHRRAGARLDVVDAMG 60  
|||||  
QY 104 RLPVDLAEEIGHRDVARYLRAAAGGTRGSNHARIDAEGPSDIPD 148  
|||||  
DB 61 RLPVDLAEEIGHRDVARYLRAAAGGTRGSNHARIDAEGPSDIPD 105  
|||||

RESULT 29  
US-08-480-810-14  
Sequence 14, Application US/08480810  
Patent No. 5801236  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,810  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-480-810-14

Query Match 70.9%; Score 105; DB 1: Length 105;  
Best Local Similarity 100.0%; Pred. No. 1,1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSARVAEELLHGAEPCADPATLTRPVHDAREGFDLTVLHRRAGARLDVVDAMG 103  
|||||  
DB 1 MMGSARVAEELLHGAEPCADPATLTRPVHDAREGFDLTVLHRRAGARLDVVDAMG 60  
|||||  
QY 104 RLPVDLAEEIGHRDVARYLRAAAGGTRGSNHARIDAEGPSDIPD 148  
|||||  
DB 61 RLPVDLAEEIGHRDVARYLRAAAGGTRGSNHARIDAEGPSDIPD 105  
|||||

RESULT 30  
US-08-508-735-14  
Sequence 14, Application US/08508735  
Patent No. 5845756  
GENERAL INFORMATION:  
APPLICANT: Stone, Steven  
APPLICANT: Jiang, Ping  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/508,735  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US to be assigned  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4848

TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-508-735-14

Query Match 70.9%; Score 105; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSARVALLLLHGAEPCADPATLTTPVHDAREGFIDTLVYLHRAGARLDVWDAMG 103  
DB 1 MMGSARVALLLLHGAEPCADPATLTTPVHDAREGFIDTLVYLHRAGARLDVWDAMG 60  
61 RLPVDLAEEELGHRDVARYLRAAAGTGRGSHNARIIDAEGPSDIPD 105

QY 104 RLPVDLAEEELGHRDVARYLRAAAGTGRGSHNARIIDAEGPSDIPD 148  
61 RLPVDLAEEELGHRDVARYLRAAAGTGRGSHNARIIDAEGPSDIPD 105

RESULT 31  
US-08-848-251-14  
Sequence 14, Application US/08848251  
Patent No. 5989815  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon Albricht, Lisa A.  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND  
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS  
TITLE OF INVENTION: GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/848,251  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/474,083  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-848-251-14

Query Match 70.9%; Score 105; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSARVALLLLHGAEPCADPATLTTPVHDAREGFIDTLVYLHRAGARLDVWDAMG 103  
DB 1 MMGSARVALLLLHGAEPCADPATLTTPVHDAREGFIDTLVYLHRAGARLDVWDAMG 60  
61 RLPVDLAEEELGHRDVARYLRAAAGTGRGSHNARIIDAEGPSDIPD 105

QY 104 RLPVDLAEEELGHRDVARYLRAAAGTGRGSHNARIIDAEGPSDIPD 148  
61 RLPVDLAEEELGHRDVARYLRAAAGTGRGSHNARIIDAEGPSDIPD 105

RESULT 32  
US-08-486-047-14  
Sequence 14, Application US/08486047  
Patent No. 5994095  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS2 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,047  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-B

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-486-047-14

Query Match  
Best Local Similarity 70.9%; Score 105; DB 2; Length 105;  
Pred. No. 1.1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMGSAVAVELLHGAEPNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVWDAMG 103  
|||||  
104 RLVPDLAEELGHRDVARYLRAAAGTGRGSHARIDAEGSPDIPD 148  
|||||  
61 RLVPDLAEELGHRDVARYLRAAAGTGRGSHARIDAEGSPDIPD 105

RESULT 33  
US-09-120-130-14  
Sequence 14, Application US/09120130  
Patent No. 6037462  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/120.130  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/480, 810  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Innen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-120-130-14

Query Match  
Best Local Similarity 70.9%; Score 105; DB 3; Length 105;  
Pred. No. 1.1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMGSAVAVELLHGAEPNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVWDAMG 103  
|||||  
104 RLVPDLAEELGHRDVARYLRAAAGTGRGSHARIDAEGSPDIPD 148  
|||||  
61 RLVPDLAEELGHRDVARYLRAAAGTGRGSHARIDAEGSPDIPD 105

RESULT 34  
US-09-115-252-14  
Sequence 14, Application US/09115252  
Patent No. 6060301  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/115,252  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/480, 810  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Innen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-115-252-14

Query Match 70.9%; Score 105; DB 3; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1,1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSAVAEILLHGAEPNCADPATLTRPVHDAAREGFDTLVYLHRAGARLDVVDAMG 103  
|||||  
Db 1 MMGSAVAEILLHGAEPNCADPATLTRPVHDAAREGFDTLVYLHRAGARLDVVDAMG 60  
|||||  
QY 104 RLVPDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIPD 148  
|||||  
61 RLVPDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIPD 105

RESULT 35  
US-08-986-515-14

Sequence 14, Application US/08986515  
Patent No. 6090578  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/986,515  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/480,810  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-986-515-14

Query Match 70.9%; Score 105; DB 3; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1,1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSAVAEILLHGAEPNCADPATLTRPVHDAAREGFDTLVYLHRAGARLDVVDAMG 103  
|||||  
Db 1 MMGSAVAEILLHGAEPNCADPATLTRPVHDAAREGFDTLVYLHRAGARLDVVDAMG 60  
|||||  
QY 104 RLVPDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIPD 148  
|||||  
Db 61 RLVPDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIPD 105

RESULT 36  
US-09-120-128-14

Sequence 14, Application US/09120128  
Patent No. 6140473  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS2 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/120,128  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,047  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:



SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-120-129-14

Query Match 70.9%; Score 105; DB 4; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSAVAEELLHGAEPCADPATLTFRPVHDAREGFLDTLVLHRAGARLDVRDAMG 103  
DB 1 MMGSAVAEELLHGAEPCADPATLTFRPVHDAREGFLDTLVLHRAGARLDVRDAMG 60

QY 104 RLPVDLAEEIGHRDVARYLRAAAGSTRGSNHARIDAEGPSDIPD 148  
DB 61 RLPVDLAEEIGHRDVARYLRAAAGSTRGSNHARIDAEGPSDIPD 105

RESULT 37

US-09-120-129-14  
Sequence 14, Application US/09120129

Patent No. 6180776

GENERAL INFORMATION:

APPLICANT: Kamb, Alexander

TITLE OF INVENTION: MTS2 GENE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

STREET: 1201 New York Avenue, Suite 1000

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/120,129

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/486,047

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: PCT/US95/03316

FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/251,938

FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,087

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,086

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,369

FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-120-129-14

Query Match 70.9%; Score 105; DB 4; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSAVAEELLHGAEPCADPATLTFRPVHDAREGFLDTLVLHRAGARLDVRDAMG 103  
DB 1 MMGSAVAEELLHGAEPCADPATLTFRPVHDAREGFLDTLVLHRAGARLDVRDAMG 60

QY 104 RLPVDLAEEIGHRDVARYLRAAAGSTRGSNHARIDAEGPSDIPD 148  
DB 61 RLPVDLAEEIGHRDVARYLRAAAGSTRGSNHARIDAEGPSDIPD 105

RESULT 38

US-09-201-139-14  
Sequence 14, Application US/09201139

Patent No. 6210949

GENERAL INFORMATION:

APPLICANT: Stone, Steven

APPLICANT: Jiang, Ping

TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

STREET: 1201 New York Avenue, Suite 1000

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/201,139

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/508,735

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/03316

FILING DATE: 17-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4848

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 105 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-201-139-14

Query Match 70.9%; Score 105; DB 4; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.1e-90;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSARVAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVBDAMG 103  
Db 1 MMGSARVAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVBDAMG 60  
QY 104 RLPVDLAEEELGHRDVARVYLRRAAGGTGSGNHARIDAEGPSDIPD 148  
Db 61 RLPVDLAEEELGHRDVARVYLRRAAGGTGSGNHARIDAEGPSDIPD 105

RESULT 39  
US-09-120-131-14  
; Sequence 14, Application US/09120131  
; Patent No. 6218146  
; GENERAL INFORMATION:  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: MTS2 GENE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/120,131  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/486,047  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: PCT/US95/03316  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/251,938  
; FILING DATE: 01-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,087  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,086  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,369  
; FILING DATE: 14-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/214,582  
; FILING DATE: 18-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24884-109348-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-8300  
; TELEFAX: 202-962-8310  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 105 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-120-131-14

Query Match 70.9%; Score 105; DB 4; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSARVAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVBDAMG 103  
Db 1 MMGSARVAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVBDAMG 60  
QY 104 RLPVDLAEEELGHRDVARVYLRRAAGGTGSGNHARIDAEGPSDIPD 148  
Db 61 RLPVDLAEEELGHRDVARVYLRRAAGGTGSGNHARIDAEGPSDIPD 105

RESULT 40  
PCT-US96-05252-5  
; Sequence 5, Application PC/TUS9605252  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: p19: A Cell Cycle Inhibitor  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Stewart Street Tower  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/05252  
; FILING DATE: Not yet assigned  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,093  
; FILING DATE: 17-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen L.  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 02307B-059910PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..157  
; OTHER INFORMATION: /note="human p16"  
PCT-US96-05252-5

Query Match 64.2%; Score 95; DB 5; Length 157;  
Best Local Similarity 100.0%; Pred. No. 3.4e-81;  
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVBDAMGRLPVDLAEEEL 113  
Db 63 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVBDAMGRLPVDLAEEEL 122  
QY 114 GHRDVARVYLRRAAGGTGSGNHARIDAEGPSDIPD 148  
Db 123 GHRDVARVYLRRAAGGTGSGNHARIDAEGPSDIPD 157

RESULT 41  
US-08-581-918A-37  
; Sequence 37, Application US/08581918A  
; Patent No. 6043030

GENERAL INFORMATION:  
APPLICANT: Beach, David H.  
APPLICANT: Demetrick, Douglas J.  
APPLICANT: Serrano, Manuel  
APPLICANT: Hannon, Gregory J.  
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley, Hoag & Elliot  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordpad  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/581,918A  
FILING DATE: 02-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/497,214  
FILING DATE: 30-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/346,147  
FILING DATE: 29-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,511  
FILING DATE: 14-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,812  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,371  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/154,915  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/991,997  
FILING DATE: 17-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-071.06  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1299  
TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 89 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-581-918A-37

Query Match 60.1%; Score 89; DB 3; Length 89;  
Best Local Similarity 100.0%; Pred. No. 7.7e-76;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IOVMMGSAVAAELLHGAEPNCADPATLTRPVHDAREGFDTLVVLRAGARLDVVD 100  
DB 1 IOVMMGSAVAAELLHGAEPNCADPATLTRPVHDAREGFDTLVVLRAGARLDVVD 60

QY 101 AMGRLPVDALEELGHRDVARYLRAAAGT 129  
DB 61 AMGRLPVDALEELGHRDVARYLRAAAGT 89

RESULT 42  
US-08-346-147B-37  
Sequence 37, Application US/08346147B  
Patent No. 6211334  
GENERAL INFORMATION:  
APPLICANT: Beach, David H.  
APPLICANT: Demetrick, Douglas J.  
APPLICANT: Serrano, Manuel  
APPLICANT: Hannon, Gregory J.  
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley, Hoag & Elliot  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordpad  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/346,147B  
FILING DATE: 29-NOV-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,511  
FILING DATE: 14-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,812  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,371  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/154,915  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/991,997  
FILING DATE: 17-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-071.04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1299  
TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 89 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-346-147B-37

Query Match 60.1%; Score 89; DB 4; Length 89;  
Best Local Similarity 100.0%; Pred. No. 7.7e-76;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IOVMMGSAVAAELLHGAEPNCADPATLTRPVHDAREGFDTLVVLRAGARLDVVD 100  
DB 1 IOVMMGSAVAAELLHGAEPNCADPATLTRPVHDAREGFDTLVVLRAGARLDVVD 60

QY 101 AMGRLPVDALEELGHRDVARYLRAAAGT 129  
DB 61 AMGRLPVDALEELGHRDVARYLRAAAGT 89

## RESULT 43

US-08-581-918A-38  
; Sequence 38, Application US/08581918A  
; Patent No. 6043030  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannon, Gregory J.  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley, Hoag & Eliot  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordpad  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/581,918A  
; FILING DATE: 02-JAN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/497,214  
; FILING DATE: 30-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/346,147  
; FILING DATE: 29-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/306,511  
; FILING DATE: 14-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/248,812  
; FILING DATE: 25-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,371  
; FILING DATE: 14-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/154,915  
; FILING DATE: 18-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/991,997  
; FILING DATE: 17-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 832-1299  
; TELEFAX: (617) 832-7000  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 88 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-581-918A-38

Query Match 48.6%; Score 72; DB 3; Length 88;  
Best Local Similarity 100.0%; Pred. No. 5.2e-60;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 IQVMMGSAFYAELLILHGAEPNCADPATLTTRPVHDAREGFLLDTLVVLRAGARLDVVD 100

Db 1 IQVMMGSAFYAELLILHGAEPNCADPATLTTRPVHDAREGFLLDTLVVLRAGARLDVVD 60  
OY 101 AMGRLPVDAE 112  
Db 61 AMGRLPVDAE 72

## RESULT 44

US-08-346-147B-38  
; Sequence 38, Application US/08346147B  
; Patent No. 6211334  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannon, Gregory J.  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley, Hoag & Eliot  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordpad  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/346,147B  
; FILING DATE: 29-NOV-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/306,511  
; FILING DATE: 14-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/248,812  
; FILING DATE: 25-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,371  
; FILING DATE: 14-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/154,915  
; FILING DATE: 18-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/991,997  
; FILING DATE: 17-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 832-1299  
; TELEFAX: (617) 832-7000  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 88 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-346-147B-38

Query Match 48.6%; Score 72; DB 4; Length 88;  
Best Local Similarity 100.0%; Pred. No. 5.2e-60;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 IQVMMGSAFYAELLILHGAEPNCADPATLTTRPVHDAREGFLLDTLVVLRAGARLDVVD 100

|||||  
Db 1 IQVMMGSAKYAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLVYVLRAGARLDVDRD 60  
OY 101 AMGRLEPVDAEE 112  
|||||  
Db 61 AMGRLEPVDAEE 72  
RESULT 45  
PCT-US96-05252-6  
; Sequence 6, Application PC/TUS9605252  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: p19: A Cell Cycle Inhibitor  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street Tower  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/05252  
; FILING DATE: Not yet assigned  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,093  
; FILING DATE: 17-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen L.  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 02307B-059910PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 136 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..136  
; OTHER INFORMATION: /note="human p15"  
PCT-US96-05252-6  
Query Match 48.6%; Score 72; DB 5; Length 136;  
Best Local Similarity 100.0%; Pred. No. 7.7e-60;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 IQVMMGSAKYAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLVYVLRAGARLDVDRD 100  
|||||  
Db 49 IQVMMGSAKYAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLVYVLRAGARLDVDRD 108  
OY 101 AMGRLEPVDAEE 112  
|||||  
Db 109 AMGRLEPVDAEE 120  
RESULT 46  
US-08-306-511A-4  
; Sequence 4, Application US/08306511A  
; Patent No. 5962316  
; GENERAL INFORMATION:

APPLICANT: Beach, David H.  
APPLICANT: Demetrick, Douglas J.  
APPLICANT: Serrano, Manuel  
APPLICANT: Hannou, Gregory J.  
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
TITLE OF INVENTION: Related Thereto  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,511A  
FILING DATE: 14-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: CSI-001CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-306-511A-4  
Query Match 48.6%; Score 72; DB 2; Length 137;  
Best Local Similarity 100.0%; Pred. No. 7.8e-60;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 IQVMMGSAKYAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLVYVLRAGARLDVDRD 100  
|||||  
Db 50 IQVMMGSAKYAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLVYVLRAGARLDVDRD 109  
OY 101 AMGRLEPVDAEE 112  
|||||  
Db 110 AMGRLEPVDAEE 121  
RESULT 47  
US-08-893-274-4  
; Sequence 4, Application US/08893274  
; Patent No. 5968821  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannou, Gregory J.  
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,  
TITLE OF INVENTION: and Uses Related Thereto  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/893,274  
FILING DATE: 15-JULY-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,511  
FILING DATE: 14-SEPTEMBER-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,812  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,371  
FILING DATE: 14-APRIL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/154,915  
FILING DATE: 18-NOVEMBER-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/991,997  
FILING DATE: 17-DECEMBER-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/963,308  
FILING DATE: 16-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-071.09  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1000  
TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-893-274-4

Query Match 48.6%; Score 72; DB 2; Length 137;  
Best Local Similarity 100.0%; Pred. No. 7.8e-60;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 41 IOVMMGSAVVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVVD 100  
DB 50 IOVMMGSAVVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVVD 109  
101 AMGRLPVLAEE 112  
110 AMGRLPVLAEE 121

RESULT 48  
US-08-474-177-16  
Sequence 16, Application US/08474177  
Patent No. 5624819  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
SOFTWARE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,177  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 138 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-177-16

Query Match 48.6%; Score 72; DB 1; Length 138;  
Best Local Similarity 100.0%; Pred. No. 7.8e-60;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 41 IOVMMGSAVVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVVD 100  
DB 51 IOVMMGSAVVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVVD 110  
101 AMGRLPVLAEE 112  
111 AMGRLPVLAEE 122

RESULT 49  
US-08-487-033-16  
Sequence 16, Application US/08487033  
Patent No. 5739027  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1E1-Beta GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:24:27 ; Search time 29.99 Seconds  
(without alignments)  
548.147 Million cell updates/sec

Title: US-09-016-869b-35

Perfect score: 148  
Sequence: 1 MEPSADWLATAARGRVEEV.....TRGSNHRARIDAEGRSPDIPD 148

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Wsize : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database :

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2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	100.0	148	16	AA81701 Multiple tumour su
2	148	100.0	148	16	AA80940 Human multiple tum
3	148	100.0	151	15	AA853401 Inhibitor of cyclin
4	148	100.0	156	16	AA85116 Cell-cycle regulat
5	148	100.0	156	20	AA24741 Human TNK-4 protei
6	148	100.0	156	21	AA188354 Human cell cycle r
7	148	100.0	391	18	AAW23354 CDK inhibitory fus
8	148	100.0	391	20	AAW95094 Human p27-p16 fus
9	148	100.0	391	21	AAW97526 Human W3 protein s
10	148	100.0	391	21	AAW96041 Antiproliferative
11	148	100.0	391	21	AAW96068 Angiogenesis inhib

12	121	81.8	156	18	AAW10627 Tumour suppressor
13	121	81.8	156	18	AAW19251 Human multiple tum
14	121	81.8	156	19	AAW74549 Amino acid sequenc
15	121	81.8	156	20	AAW40524 Human MTSL protein
16	121	81.8	156	19	AAW80524 A human multiple t
17	121	81.8	156	21	AAW15498 Human MTSL protein
18	121	81.8	156	21	AAW97524 Human p16 protein
19	121	81.8	156	21	AAW96053 Human cyclin depen
20	121	81.8	156	21	AAW96067 Human cyclin depen
21	121	81.8	156	21	AAW92921 Human multiple tum
22	121	81.8	156	21	AAW91102 Human multiple tum
23	121	81.8	156	21	AAW59415 Human MTSL protein
24	121	81.8	156	21	AAW54902 Human multiple tum
25	121	81.8	156	22	AAU02122 Human multiple tum
26	121	81.8	156	22	AAE01002 Human multiple tum
27	121	81.8	156	22	AAW67334 Protein encoded by
28	121	81.8	156	22	AAW68890 Human Multiple Tum
29	121	81.8	228	21	AAW97522 Human W3 protein s
30	121	81.8	228	21	AAW6051 Antiproliferative
31	121	81.8	228	21	AAW6078 Angiogenesis inhib
32	121	81.8	237	20	AAW95105 Human W9 protein s
33	121	81.8	237	21	AAW97534 Human W9 protein s
34	121	81.8	237	21	AAW6049 Angiogenesis inhib
35	121	81.8	237	21	AAW6076 Angiogenesis inhib
36	121	81.8	252	20	AAW95106 Truncated p27/p16
37	121	81.8	252	21	AAW97535 Human W10 protein
38	121	81.8	252	21	AAW96050 Antiproliferative
39	121	81.8	252	21	AAW96077 Angiogenesis inhib
40	121	81.8	323	21	AAW96079 Secretable angio
41	121	81.8	334	20	AAW95103 Truncated p27/p16
42	121	81.8	334	20	AAW97532 Human W8 protein s
43	121	81.8	334	21	AAW6047 Antiproliferative
44	121	81.8	334	21	AAW6074 Angiogenesis inhib
45	121	81.8	365	18	AAW23536 CDK inhibitory fus
46	121	81.8	365	20	AAW95107 Human p16p27 fusio
47	121	81.8	365	20	AAW95096 Human p16p27 fusio
48	121	81.8	365	21	AAW97527 Human W4 protein s
49	121	81.8	365	21	AAW97529 Human W4 protein s
50	121	81.8	365	21	AAW96042 Antiproliferative
51	121	81.8	365	21	AAW96044 Angiogenesis inhib
52	121	81.8	365	21	AAW96069 Angiogenesis inhib
53	121	81.8	365	21	AAW96071 Angiogenesis inhib
54	121	81.8	380	18	AAW23535 CDK inhibitory fus
55	121	81.8	380	20	AAW95095 Human p16(GS)p27 f
56	121	81.8	380	21	AAW97528 Human W5 protein s
57	121	81.8	380	21	AAW96043 Antiproliferative
58	121	81.8	380	21	AAW96070 Angiogenesis inhib
59	120	81.1	337	21	AAW96080 Secretable angio
60	115	77.7	172	22	AAU02966 Angiogenesis conver
61	112	75.7	156	22	AAE01008 Human multiple tum
62	105	70.9	105	16	AAW81700 Multiple tumour su
63	105	70.9	105	16	AAW80947 Human multiple tum
64	105	70.9	105	18	AAW19254 Human multiple tum
65	105	70.9	105	19	AAW74550 Amino acid sequenc
66	105	70.9	105	19	AAW40525 Human MTSL-beta
67	105	70.9	105	20	AAW80525 A human multiple t
68	105	70.9	105	21	AAW15500 Human MTSLbeta p
69	105	70.9	105	21	AAW92922 Human multiple tum
70	105	70.9	105	21	AAW91103 Human MTSLbeta
71	105	70.9	105	21	AAW59416 Human MTSLbeta p
72	105	70.9	105	22	AAW54903 Human multiple tum
73	105	70.9	105	22	AAU02123 Human multiple tum
74	105	70.9	105	22	AAE01004 Human multiple tum
75	105	70.9	105	22	AAW67335 MTSLbeta protein

#### ALIGNMENTS

RESULT 1  
AA81701 standard; Protein; 148 AA.  
XX

AC	AAR81701:
XX	
DT	08-MAY-1996 (first entry)
XX	
DE	Multiple tumour suppressor 1 (MTS1) polypeptide.
XX	
KM	Multiple tumour suppressor: MTS1; cancer: diagnosis; assay:
KM	predisposition; melanoma; leukaemia; lymphoma; prognosis;
KM	pancreas; breast; thyroid.
XX	
OS	Homo sapiens.
XX	
PN	W09525813-A1.
XX	
PD	28-SEP-1995.
XX	
PF	17-MAR-1995; 95WO-US03537.
XX	
PR	01-JUN-1994; 94US-0251938.
XX	
PR	18-MAR-1994; 94US-0214582.
XX	
PR	18-MAR-1994; 94US-0215086.
XX	
PR	18-MAR-1994; 94US-0215087.
XX	
XX	14-APR-1994; 94US-0227369.
XX	
PA	(MYRI-) MYRIAD GENETICS INC.
PA	(UTAH) UNIT UTAH RES FOUND.
XX	
PI	Cannon-Albright LA, Kamb A, Skolnick MH:
XX	
DR	WPI: 1995-344626/44.
DR	N-PSDB; AAT00736.
XX	
PT	Detecting polymorphism associated with cancer pre:disposition - also
PT	DNA, vectors and host cells e.g. for gene or protein replacement
PT	therapy and drug screening
XX	
PS	Example 8; Pages 92-93; 148pp; English.
XX	
CC	An individual can be diagnosed as having a predisposition to cancer
CC	by detecting an alteration in the wild type multiple tumour
CC	suppressor (MTS) gene, using gene probes which hybridise to the MTS1
CC	gene ORF AAT00736 (which encodes AAR81701) mutant sequences AAT00749/50.
CC	The above assay can also be used in the diagnosis and prognosis of
CC	melanoma, lymphoma, leukaemia and pancreas, breast and thyroid
CC	cancers, etc..
XX	
SQ	Sequence 148 AA:
XX	
XX	Very Match 100.0%; Score 148; DB 16; Length 148;
XX	Best Local Similarity 100.0%; Pred. No. 1.5e-134; Mismatches 0; Indels 0; Gaps 0
XX	Matches 148; Conservative 0;
QY	1 MEPSADWLATAAARGVEEVRALLLEAVAPNPNSTYGRRIQVMMGASRAVELLLHGA 60
DB	1 MEPSADWLATAAARGVEEVRALLLEAVAPNPNSTYGRRIQVMMGASRAVELLLHGA 60
QY	61 EENCADPALITRPVINDAAREGFLLDITLVVLRHAGARLDVDAWGRLPVDLAELGHRDVAR 120
DB	61 EENCADPALITRPVINDAAREGFLLDITLVVLRHAGARLDVDAWGRLPVDLAELGHRDVAR 120
QY	121 YLRNAAAGTGRGSHARIDAAEGRSPDIP 148
DB	121 YLRNAAAGTGRGSHARIDAAEGRSPDIP 148
XX	
XX	AAAR80940 standard; Protein: 148 AA.
XX	
XX	AAAR80940;
DT	03-MAY-1996 (first entry)

```

XX DE Human multiple tumour suppressor polypeptide, MTS1.
XX XX
XX KW Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;
XX KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;
XX KW gene therapy; chronic.
XX OS
XX OS Homo sapiens.
XX PN
XX PN W09525429-A1.
XX PD
XX PD 28-SEP-1995.
XX PF
XX PF 17-MAR-1995; 95WO-US03316.
XX XX
XX PR 01-JUN-1994; 94US-0251938.
XX PR 18-MAR-1994; 94US-0214581.
XX PR 18-MAR-1994; 94US-0214582.
XX PR 18-MAR-1994; 94US-0215088.
XX PR 14-APR-1994; 94US-0227369.
XX PR 18-MAR-1994; 94US-0215086.
XX PR 18-MAR-1994; 94US-0215087.
XX PA
XX PA (MYRI-) MYRIAD GENETICS INC.
XX PI
XX PI Kamb A;
XX XX
XX DR WPI; 1995-344401/44.
XX DR N-PSDB; AAQ9158.
XX XX
XX PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences
XX PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.
XX PT melanoma or leukaemia
XX PS
XX PS Claim 5; Page 92-93; 156pp; English.
XX CC
XX CC Several multiple tumour suppressor (MTS) polypeptides have been
XX CC isolated and sequenced. This sequence is the MTS polypeptide MTS1
XX CC MTS polypeptide-encoding cDNAs and mutants of these are useful for
XX CC the diagnosis or prognosis of human cancer. Germ-line mutations of
XX CC MTS cDNAs can be used for diagnosing predisposition to melanoma,
XX CC leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's
XX CC lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus,
XX CC testis, kidney, stomach and rectum. The wild-type gene is useful
XX CC for gene therapy and MTS polypeptides may also be used for protein
XX CC replacement therapy. Also the polypeptides or cells contg. an
XX CC altered MTS gene are useful for screening for potential cancer
XX CC therapeutics.
XX XX
XX SQ Sequence 148 AA;
XX XX
XX Query Match 100.0%; Score 148; DB 16; Length 148;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-134;
XX Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MEPSADWLTAARGRVEEVRALLLEAVLNPAPNSTYGRPPVMMGSAVALLLHGA 60
DB 1 MEPSADWLTAARGRVEEVRALLLEAVLNPAPNSTYGRPPVMMGSAVALLLHGA 60
QY 61 EPNCDPATLTTPVNDAAEGFLDTLTVYVHRGARGRLVDADWGRLPVDLAEPLGHRDVAR 120
DB 61 EPNCDPATLTTPVNDAAEGFLDTLTVYVHRGARGRLVDADWGRLPVDLAEPLGHRDVAR 120
QY 121 YLRAAAGGTGRGSHARIDAEGSPDIPD 148
DB 121 YLRAAAGGTGRGSHARIDAEGSPDIPD 148
XX
XX RESULT 3
XX ID AAR53401 standard; Protein; 151 AA.
XX XX

```



DT	23-AUG-1999	(first entry)
XX		
DE	Human INK-4 protein p16.	
XX		
KW	INK-4; p16; p15; p18; p19; CDK4; cell cycle regulatory protein;	
KW	transgenic mouse; p16-INK4-a; carcinogen; anti-proliferative.	
XX		
OS	Homo sapiens.	
XX		
PN	US591997-A.	
XX		
PD	06-JUL-1999.	
XX		
PE	04-APR-1996;	9605-0627610.
XX		
PR	04-APR-1996;	9605-0627610.
PR	18-NOV-1993;	9305-0154915.
PR	14-APR-1994;	9405-0227371.
PR	25-MAY-1994;	9405-0248812.
PR	14-SEP-1994;	9405-0306311.
PR	29-NOV-1994;	9405-0346147.
PR	30-JUN-1995;	9505-0497214.
PR	02-JAN-1996;	9605-0581918.

PA (COLD- ) COLD SPRING HARBOR LAB.  
PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.  
XX  
XX  
PI Beach DH, DePinho RA, Serrano M;  
XX  
XX WPI: 1999-394656/33.  
DR N-PSDB: AAX80472.  
XX  
XX Transgenic mice with modified cell-cycle regulation  
XX  
XX Disclosure: Column 45-46; 35pp; English.

CC The present invention describes a transgenic mouse having germline and  
CC somatic cells which comprise an incorporated transgene that disrupts and  
CC inhibits the p16-INK4-a gene leading to tumour susceptibility. Also  
CC described is a method of making a mouse and mouse embryonic stem cells a  
CC functionally disrupted p16-INK4-a gene which comprises transferring a  
CC transgene construct into embryonic stem cells of a mouse and  
CC transferring these into a mouse blastocyst and implanting the resulting  
CC chimeric blastocyst into a female mouse selecting offspring having an  
CC endogenous p16-INK4-a gene allele. The transgenic mouse is useful for  
CC evaluating the carcinogenic potential or the anti-proliferative activity  
CC of a test compound. The present sequence represents the human INK4  
CC protein p16 given in the present invention.

Sequence 156 AA;

Query Match	100.0%	Score 148;	DB 20;	Length 156;
Best Local Similarity	100.0%;	Pred. No. 1.6e-134;		
Matches 148; Conservative	0;	Mismatches	0;	Indels 0;
		Gaps	0	

QY 1 MESSAWLTAAARBEVEVEVALLLEAVLLEPNRAANSNGRRP IQYMMAGSRAVELLLHGA 60  
9 mepsawwltaaariveevallleavallpnapsy9grppiqymmgasravellllhga 68  
Db  
61 EPNCADPATLTPRVDAAREGFLDTLVVLRHAGARLDVRDANGRLPVDLAEELGHRDVAR 120  
QY  
69 epncadpatltprvdaaregflfcltvlvlnnagarldvdvdaagrlpvdlaeelgrrdvar 128  
pb

QY 121 YLRAAGGTRGSNHARIDAEGPSDIPD 148

Db 129 ylraaagtrqsnharidaaeppsdiid 156

```

RESULT      6
AAY88354
ID  AAY88354 standard; Protein; 156 AA
XX

```

AC MAY88354;

DT 14-JUL-2000 (first entry)

Human cell cycle regulatory protein p16 amino acid sequence.

Cell cycle regulatory protein; CCR; p16; diagnostic assay; detection;  
cell proliferation; differentiation; neoplasia; cancer; cell growth;  
cyclin-dependent kinase inhibitor; CDK; human; chromosome 9p21-22.

OS Homo sapiens.

PN US6043030-A

PD 28-MAR-2000

PF 02-JAN-1996; 96US-0581918.

PR 17-DEC-1992; 92US-0991997.

PR 14-APR-1994: 94US-0227371.

14-SEP-1994: 94US-0306511.

PR 30-JUN-1995: 95JIS-0497214

AA  
PA (COLD-) COLD SPRING HARBOR LAB

PI Beach DH, Demetrick DJ, Serrano M, Hannon GT; AA

WPT: 2000-270336/23

DN IN-PSDB; AAAA13050 :  
XX

PT Use of a manual lift  
device in a dis-

PI disorder character

XX  
XX  
14  
13  
12  
11  
10  
9  
8  
7  
6  
5  
4  
3  
2  
1

CC This sequence represents the human cell cycle regulatory protein (CCR  
CC p16 amino acid sequence. The p16 gene is located on chromosome 9p21-22.  
CC The invention relates to a diagnostic assay which comprises detecting a  
CC mutation in the p16 gene, which is used to identify a cell or cells at  
CC risk of developing a disorder characterised by unwanted cell

CC (CDK)-inhibitory protein, and functions as an inhibitor of cell-cycle

CC identifying a cell or cells at risk for a disorder (neoplasia)

CC method is used for detecting mutations in either a CCR gene or CDK gene characterized by unbalanced cell proliferation. The

also used for detecting mutations in other cellular proteins which

CC disrupt protein interactions which disrupt binding  
CC the p53 protein with other cellular proteins  
CC the p53 protein with other cellular proteins

CC suppressor protein Wt1. They can also be used to detect mutations in

CC cellular proteins which interact with ras, e.g. ras GTPase activating

CC genes encoding proteins which are unable to physically interact with

XX

**SQ** Sequence 156 AA;

Query Match	100.0%;	Score 148;	DB 21;	Length 156;
Best Local Similarity	100.0%;	Pred. No. 1.6e-134;		
Matches 148; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

**QY** 1 M P S A D W L A T A A R G R V E E V R A L L E A V A L P N A P N S Y G R P I Q V M M G S A R V A E L L L H G A 60  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
**Db** 9 m e p s d w l a t a a r g r v e e v r a l l e a v a l n a p n s y g r i p i q v m m g s a r v a e l l l h g a 68

QY 61 EPNCADPATITRPVHDAAREGFLDTLVVLRAGARLDVDAWGRLPVDLAELGHRDVAR 120  
 |||||||  
 Db 69 epncadpatittrpvhdaaregfltdltvlhragardvrdawgripvdlaeelghrdvar 128  
 QY 121 YLRAAAGGTRGSNHARIDAAEGSPDIP 148  
 |||||||  
 Db 129 YLRAAAGGTRGSNHARIDAAEGSPDIP 156

RESULT 7  
 AAM23534  
 ID AAM23534 standard; Protein: 391 AA.  
 AC AAM23534;  
 DT 16-MAR-1998 (first entry)  
 XX  
 DE CDK inhibitory fusion protein #1.  
 KW Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gene;  
 K chimeric polypeptide; human; binding motif; proliferation control;  
 K cell differentiation; cell-cycle inhibitor; proliferative disorder;  
 KW tissue degeneration; therapy.  
 XX  
 OS Homo sapiens.  
 EH Key Location/Qualifiers  
 FT Misc-difference 1..7  
 FT /note= "poly-His tag"  
 FT Misc-difference 205..219  
 FT /note= "(GlySer)2 linker"  
 FT  
 XX WO9727297-A1.  
 XX 31-JUL-1997.  
 PD 17-JAN-1997; 97WO-US00569.  
 PF 23-JAN-1996; 96US-0589981.  
 PR  
 XX (MITO-) MITOTIX INC.  
 PA Beach D, Gyuris J, Lamphere L;  
 PI WPI: 1997-393685/36.  
 DR N-PSDB; AAT74051.  
 XX  
 PT Chimeric inhibitor of cyclin dependent kinase - useful for gene  
 P therapy of cancer and other proliferative and differentiative  
 P diseases  
 XX  
 PS Claim 40; Page 38-40; 58pp; English.  
 XX  
 CC This sequence represents a chimeric polypeptide of the invention. It was  
 CC derived from a fusion of the human p27 and p16 cDNA sequences. The  
 CC chimeric polypeptides of the invention have cyclin-dependent kinase (CDK)  
 CC binding motifs from at least two different proteins that bind to CDKs.  
 CC The protein controls proliferation and/or differentiation of cells,  
 CC particularly they inhibit cell-cycle progression. They can be used to  
 CC treat a wide range of proliferative disorders, e.g. cancer, leukaemia,  
 CC psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They  
 CC can also treat diseases associated with de-differentiation or  
 CC degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's  
 CC diseases, gastric ulcers and autonomous diseases of the peripheral  
 CC nervous system. Other applications include reducing growth of hair and  
 CC protecting hair follicle cells against cytotoxic treatments, cosmetically  
 CC to treat various forms of folliculitis, and to inhibit spermatogenesis or  
 CC oogenesis. The chimeric proteins can also be used in vitro to maintain  
 CC cells, especially neurons intended for testing specific activity of  
 CC trophic factors, at selected points in the cell cycle. The proteins are  
 CC more active inhibitors of the CDK/cyclin complex than binding motifs used  
 CC individually (since they may bind to CDK involved in different stages of  
 CC the cell cycle).

XX  
 SQ Sequence 391 AA;  
 Query Match 100.0%; Score 148; DB 18; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 3,8e-134;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAARGVEEYRALLEAVLPNAPNSYGRRPICVMMMGSAVALLHGA 60  
 |||||||  
 Db 244 mepsadwlataaargveeyrallaevalpnpnsgyrrpdygmungsarvaellllhhga 303  
 QY 61 EPNCADPATITRPVHDAAREGFLDTLVVLRAGARLDVDAWGRLPVDLAELGHRDVAR 120  
 |||||||  
 Db 304 epncadpatittrpvhdaaregfltdltvlhragardvrdawgripvdlaeelghrdvar 363  
 QY 121 YLRAAAGGTRGSNHARIDAAEGSPDIP 148  
 |||||||  
 Db 364 YLRAAAGGTRGSNHARIDAAEGSPDIP 391

RESULT 8  
 AAM95094  
 ID AAM95094 standard; Protein: 391 AA.  
 AC AAM95094;  
 DT 25-MAY-1999 (first entry)  
 XX  
 DE Human p27-p16 fusion protein.  
 XX  
 KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;  
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;  
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;  
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;  
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;  
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;  
 KW tachycardia; human; p27; p16.  
 XX  
 OS Homo sapiens.  
 OS  
 XX WO9906540-A2.  
 XX 11-FEB-1999.  
 PD 29-JUL-1998; 98WO-US15759.  
 PF 29-JUL-1997; 97US-0902572.  
 PR  
 XX (MITO-) MITOTIX INC.  
 PA Beach DH, Gyuris J, Lamphere L;  
 PI WPI: 1999-153770/13.  
 DR N-PSDB; AAX26220.  
 XX  
 PT Fusion and chimaeric proteins including cyclin-dependent kinase  
 P binding motif - used for regulation of cell proliferation and  
 P differentiation, for treatment of, e.g. vascular injury, cancers,  
 P fibrosis and neurodegeneration  
 XX  
 PS Claim 63; Page 70-72; 88pp; English.  
 XX  
 CC The invention relates to novel inhibitors of cyclin-dependent kinases  
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant  
 CC transfection system (A) that comprises: (i) first gene construct  
 CC comprising a sequence encoding an inhibitory polypeptide containing at  
 CC least one CDK-binding motif for binding and inhibiting activity of a CDK,  
 CC linked to a transcription regulator functional in eukaryotic cells; (ii)  
 CC second gene construct comprising a sequence encoding a polypeptide that  
 CC promotes endothelialisation, and (iii) a gene delivery composition for  
 CC delivering the GCs to a cell for transfection. Also provided are nucleic  
 CC acids encoding a fusion protein (FP) containing: (i) a therapeutic

CC polypeptide sequence (TP) from an intracellular protein that alters a  
 CC cellular process when FP enters the cell, and (ii) a transcellular  
 CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP  
 CC consists of at least one CDK-binding motif and a TCP. (A) are used to  
 CC treat vascular wounds that involve a break in the endothelium and  
 CC excessive proliferation of smooth muscle, particularly restenosis but  
 CC more generally any repair of cardiovascular damage, arteriosclerotic  
 CC lesions or for endothelialisation of synthetic vascular grafts. More  
 CC generally, FP are used to treat unwanted cellular proliferation in a very  
 CC wide range of situations, e.g. for treating vascular diseases as above;  
 CC fibrotic disorders (e.g. rheumatoid arthritis, diabetes, cirrhosis); many  
 CC tumours (gliomas, leukemias); chronic inflammation; neurodegeneration;  
 CC acne; also to control hair growth (e.g. to prevent hair loss caused by  
 CC chemotherapy or radiation); periodontal disease; to treat tachycardia;  
 CC to inhibit spermatogenesis etc. Chimeric proteins comprising CDK-binding  
 CC motifs from two or more different proteins bind to CDKs so inhibit cell  
 CC cycle progression, particularly smooth muscle cell proliferation. The  
 CC gene constructs may also be used to produce FP in cell cultures, for  
 CC production or for regulating cell differentiation in vitro. The present  
 CC sequence represents a human p27-p16 fusion protein.

Sequence 391 AA:

Query Match 100.0%; Score 148; DB 20; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-134;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALLLEAVLPPNAPNSYGRRPQVMMGSAARVAELLHLGA 60  
 DB 244 mepsadwlataaargveevrallleavlpnapnsygrripqvmmgssarvaeellllhga 303  
 QY 61 EPNCADPATLTFRVYHDAAREGFLDTLVYLHRAGARLDVNDAGRLPYDLAEELGHRDVAR 120  
 DB 304 epcnccdpattltfrvphdaaregfdltlvylhragarldvndagrlpydlaeelghrdvar 363  
 QY 121 YLRAAGGTGRGSHNARIDAAEGPSDIPD 148  
 DB 364 ylraaaggtgrgshnaridaaegpsdipd 391

RESULT 9

AA97526 AAY97526 standard; Protein; 391 AA.

XX AAY97526;

XX 15-JAN-2001 (first entry)

XX Human W3 protein sequence.

KW Human: chimeric cyclin dependent kinase inhibitor; CDK1; therapy;  
 KW adenovirus E4 protein; neoplasia; W3 protein.

OS Homo sapiens.

PN WO200052184-A1.

PD 08-SEP-2000.

PF 01-MAR-2000; 2000WO-US05350.

PR 01-MAR-1999; 99US-0122974.

PR 08-APR-1999; 99US-0128271.

PR 09-APR-1999; 99US-0128515.

PA (CELL-) CELL GENESYS INC.

PI (MITO-) MITOTIX INC.

PI Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;  
 DR WPI: 2000-587315/55.  
 DR N-PSDB: /AAA90923.

XX protein and nucleic acid compositions for preventing and treating  
 PT neoplasias (particularly cancer), comprises a novel chimeric cyclin  
 PT dependent kinase inhibitor and adenovirus E4 protein -  
 PS Example 1; Page 108-109; 126pp; English.

XX This sequence represents the human W3 protein.  
 CC The invention relates to a protein composition comprising a novel  
 CC purified chimeric cyclin dependent kinase inhibitor (CDK1) and a  
 CC or the DNA encoding it are useful for treating neoplasias in animals. The  
 CC compositions also find use in assays to eliminate a specific  
 CC sub-population of cultured cells, to determine the susceptibility of  
 CC neoplastic cells to treatment with the compositions and also in assays to  
 CC synchronise cell growth in cultured cells.

SQ Sequence 391 AA:

Query Match 100.0%; Score 148; DB 21; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-134;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALLLEAVLPPNAPNSYGRRPQVMMGSAARVAELLHLGA 60  
 DB 244 mepsadwlataaargveevrallleavlpnapnsygrripqvmmgssarvaeellllhga 303  
 QY 61 EPNCADPATLTFRVYHDAAREGFLDTLVYLHRAGARLDVNDAGRLPYDLAEELGHRDVAR 120  
 DB 304 epcnccdpattltfrvphdaaregfdltlvylhragarldvndagrlpydlaeelghrdvar 363  
 QY 121 YLRAAGGTGRGSHNARIDAAEGPSDIPD 148  
 DB 364 ylraaaggtgrgshnaridaaegpsdipd 391

RESULT 10

AA96041 AAY96041 standard; Protein; 391 AA.

XX AAY96041;

XX 05-DEC-2000 (first entry)

XX Antiproliferative p27-p16 fusion protein W3.

XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; p27; INK4;

KW p16; human; smooth muscle cell; hyperproliferation; restenosis;  
 KW vasotropic; antiproliferative; gene therapy.

OS Homo sapiens.  
 OS Synthetic.

PH Key Location/Qualifiers

FT Peptide 1..7 /label= 6His\_tag

FT Protein 8..204 /label= p27

FT Peptide 205..219 /label= Hinge

FT Protein 239..391 /label= p16

PN WO200052159-A1.

PD 08-SEP-2000.

PF 28-FEB-2000; 2000WO-US04971.

PR 01-MAR-1999; 99US-0122974.

PR 05-NOV-1999; 99US-0163682.  
 PR 09-DEC-1999; 99US-0457568.

```

XX (CELL-) CELL GENESYS INC.
PA (MITO-) MITOTIX INC.
XX Mcarthur J, Gyuris J, Finer M;
XX WPI: 2000-594183/56.
DR N-PSDB; AAA50488.
PT Novel recombinant lentivirus for inhibiting proliferation of smooth
PT muscle cells in e.g. restenosis, is replication deficient and comprises
PT a transgene encoding a cyclin dependent kinase inhibitor -
XX
XX Example 1; Page 101-103; 126pp; English.
XX
XX The present sequence is that of p27-p16 fusion protein W3 comprising
XX an N-terminal 6His tag, the human p27 protein (see AAY96052), a
XX (Gly4Ser)3 hinge and the human p16 protein (see AAY96053). It is
XX encoded by a nucleic acid obtained by PCR amplification of p27 and
XX p16 DNAs using primers that also included codons for the tag/hinge
XX regions. A claimed method for inhibiting smooth muscle cell
XX hyperproliferation involves transducing smooth muscle cells with a
XX replication-deficient recombinant adenovirus that lacks functional
XX E1 and E4 regions, and comprises a transgene encoding a cyclin
XX dependent kinase inhibitor (CDK1). The CDK1 is selected from an
XX INK4 family protein such as human p16, a CIP/KIP family protein
XX such as p27, active fragments of these, or fusion proteins
XX comprising (active fragments of) an INK4 family protein and a
XX CIP/KIP family protein (see AAY96046 and AAY96049). The method is used
XX to inhibit mammalian smooth muscle cell hyperproliferation, induced
XX by injury caused by angioplasty, stent placement or vein
XX engraftment. It is useful for treating vascular pathologies e.g.,
XX restenosis. Also claimed are recombinant lentiviruses encoding
XX CDK1s.
XX
XX Sequence 391 AA:
SQ

```

```

XX Key Location/Qualifiers
FH Peptide 1..7
FT /label= 6His_tag
FT 8..204
FT Protein /label= p27
FT 205..219
FT Peptide /label= Hinge
FT 239..391
FT Protein /label= p16
XX
XX WO200052158-A1.
XX
XX 08-SEP-2000.
XX
XX 28-FEB-2000; 2000WO-US04970.
XX
XX 01-MAR-1999; 99US-0122974.
XX 05-NOV-1999; 99US-0163682.
XX 09-DEC-1999; 99US-0457646.
XX
XX (CELL-) CELL GENESYS INC.
PA (MITO-) MITOTIX INC.
XX
XX Patel S, Mcarthur J, Gyuris J;
XX
XX WPI: 2000-565501/52.
XX N-PSDB; AAA50523.
XX
XX The present sequence is that of p27-p16 fusion protein W3
XX comprising an N-terminal 6His tag, the human p27 protein (see
XX AAY96066), a (Gly4Ser)3 hinge, and the human p16 protein (see
XX AAY96067). The fusion protein is encoded by a nucleic acid (see
XX AAA50523) that was obtained by PCR amplification of human p27 and p16
XX DNAs using primers that also included codons encoding the tag/hinge
XX regions of the fusion protein. A claimed method for inhibiting
XX angiogenesis involves transducing an epithelial cell with a
XX transgene encoding a cell dependent kinase inhibitor (CDK1). The
XX delivery system for the transgene is a liposome or a recombinant
XX virus. The CDK1 is a protein of the CIP/KIP family such as p27, a
XX protein of the INK4 family such as p16, active fragments of these
XX proteins, or a fusion of 2 CDK1 proteins such as p27 and p16. The
XX method is useful in treating conditions associated with angiogenesis,
XX such as neoplasia, rheumatoid arthritis, endometriosis, psoriasis
XX and vascular retinopathy (claimed). Alternatively, the transgene
XX is delivered to an auxiliary cell, and is expressed by that cell
XX such that the CDK1 is released into the blood and contacts the
XX target epithelial cell. The p27-p16 fusion proteins interact with
XX CDK4/cyclinD, CDK2/cyclinA and CDK2/cyclinE and inhibit cell cycle
XX progression.
XX
XX Sequence 391 AA:
SQ

```

XX Homo sapiens.  
 OS Synthetic.

OY 121 YLRAAGGTRGSHARIDAEGSPDIP 148  
 ||||||||||||||||||  
 Db 364 YLRAAGGTRGSHARIDAEGSPDIP 391

## RESULT 12

AAW10627  
 ID AAW10627 standard; Protein; 156 AA.

AC AAW10627;

DT 28-OCT-1997 (first entry)

DE Tumour suppressor p16.

KM Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;  
 cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;  
 anti-angiogenic activity; hyperproliferative disorder.

OS Homo sapiens.

WO9703635-A2.

PD 06-FEB-1997.

PF 17-JUL-1996; 96WO-US11787.

PR 17-JUL-1995; 95US-0502881.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Jin X, Roth J;

DR WPI: 1997-132336/12.

N-PSDB; AAT60951.

PT Expression construct contg. DNA for tumour suppressor p16 - to  
 restore p16 activity to transformed cells, useful for treating lung  
 or bladder cancer or melanoma

PS Disclosure: Fig 1b; 92pp; English.

XX This sequence represents the tumour suppressor p16. The DNA encoding  
 CC this sequence is joined to a promoter functional in eukaryotic cells and  
 CC used in the expression construct of the invention. p16 is an inhibitory  
 CC subunit, which is involved in the control of cyclin-dependent kinase 4  
 CC activity, and functions as a tumour suppressor. By detecting this  
 CC sequence or the DNA encoding it, cancer cells can be detected. When the  
 CC nucleic acid molecule is in the sense orientation, the expression  
 CC construct can be used to restore p16 function in a cell, particularly by  
 CC reversing the transformed phenotype in tumours, especially lung or  
 CC bladder cancer or melanoma. It may also have anti-angiogenic activity,  
 CC and inhibit hyperproliferative disorders, e.g. restenosis. When the  
 CC nucleic acid molecule is inserted in the antisense orientation the  
 CC expression construct inhibits p16 function. Reduced or increased levels  
 CC of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by  
 CC Southern or Northern blot, antibody immunoblot, fluorescent cell sorting  
 CC or immunoassay.

SO Sequence 156 AA.

## Query Match

Best Local Similarity 81.8%; Score 121; DB 18; Length 156;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 ALPNAPNSYGRPIQVMMGSAFYAEELLHGAEPNCADPATLTPVHDAREGFLDTLV 87  
 ||||||||||||||||||  
 Db 36 alpnapnsygrripqymmmgsarvaeellllhgaepncadpatlttrpvhdaregfltdtlv 95  
 OY 88 VLHRAGARLDVDRAMGRPLVVDLAEEIGHRDVARYLRAAAGGTRGSHARIDAEGSPDIP 147  
 ||||||||||||||||||  
 Db 96 vlhragarldvdrdwgrlplvdlaeelghrdvarylraaaggttrgsnharidaaegpsdip 155

OY 148 D 148  
 |  
 Db 156 d 156

## RESULT 13

AAW19251  
 ID AAW19251 standard; Protein; 156 AA.

AC AAW19251;

DT 10-SEP-1997 (first entry)

DE Human multiple tumour suppressor 1 gene product.

KM Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis.  
 OS Homo sapiens.

US5624819-A.

PD 29-APR-1997.

PF 18-MAR-1994; 94US-0214582.

PR 07-JUN-1995; 95US-0474177.

PR 18-MAR-1994; 94US-0214582.

PR 18-MAR-1994; 94US-0215086.

PR 18-MAR-1994; 94US-0215087.

PR 14-APR-1994; 94US-0227369.

PR 01-JUN-1994; 94US-0251938.

PR 17-MAR-1995; 95WO-US03537.

PA (MYRI-) MYRIAD GENETICS INC.

PI (UTAH ) UNIV UTAH RES FOUND.

PI Cannon-Albright LA, Kamb A, Skolnick MH;

DR WPI: 1997-258217/23.

N-PSDB; AAT72311.

PT Human mutant multiple tumour suppressor gene sequences - for  
 production of recombinant mutant polypeptide(s)

PS Claim 1: Columns 61-64; 72pp; English.

XX The present sequence the human multiple tumour suppressor 1  
 CC (MTS1) gene product, useful in cancer diagnosis.

SO Sequence 156 AA;

## Query Match

Best Local Similarity 81.8%; Score 121; DB 18; Length 156;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 ALPNAPNSYGRPIQVMMGSAFYAEELLHGAEPNCADPATLTPVHDAREGFLDTLV 87  
 ||||||||||||||||||  
 Db 36 alpnapnsygrripqymmmgsarvaeellllhgaepncadpatlttrpvhdaregfltdtlv 95  
 OY 88 VLHRAGARLDVDRAMGRPLVVDLAEEIGHRDVARYLRAAAGGTRGSHARIDAEGSPDIP 147  
 ||||||||||||||||||  
 Db 96 vlhragarldvdrdwgrlplvdlaeelghrdvarylraaaggttrgsnharidaaegpsdip 155  
 OY 148 D 148  
 |  
 Db 156 d 156  
 RESULT 14  
 AAW74549  
 ID AAW74549 standard; Protein; 156 AA.



```

XX AAW74549;
AC 04-DEC-1998 (first entry)
DT
XX
XX Amino acid sequence of multiple tumour suppressor 1.
DE
XX Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
KW somatic mutation; gene therapy.
XX
XX Homo sapiens.
OS
XX US5801236-A.
PN
XX 01-SEP-1998.
PD
XX
XX 07-JUN-1995; 95US-0480810.
PF
XX
PR 07-JUN-1995; 95US-0480810.
PR 18-MAR-1994; 94US-0214582.
PR 18-MAR-1994; 94US-0215086.
PR 18-MAR-1994; 94US-0215087.
PR 14-APR-1994; 94US-0227369.
PR 01-JUN-1994; 94US-0251938.
PR 17-MAR-1995; 95WO-US03316.
XX
XX (MYRI-) MYRIAD GENETICS INC.
PA
XX
XX Kamb A;
PI
XX
XX WPI: 1998-494842/42.
DR N-PSDB; AAV53819.
XX
XX Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT useful as hybridisation probes, primers and recombinant production
PT of MTS in the diagnosis and treatment of cancers related to MTS
PT mutation(s)
XX
XX Disclosure; Column 63-64; 73pp; English.
XX
XX This is the amino acid sequence of the multiple tumour suppressor 1
CC (MTS-1) protein, used in the method of the invention. The MTS gene
CC is useful in the diagnosis and prognosis of human cancer. e.g. by
CC standard nucleic hybridisation techniques, of patient samples. The
CC mutated sequences are those that are present in somatic mutations
CC of the gene in cancers. The vectors can be used for gene therapy
CC strategies to replace function of mutated protein in patients. These
CC can also be used to construct protein mimetics, also for therapeutic
CC strategies. In addition the expression constructs can also be used
CC for recombinant production of MTS. Recombinant MTS can be used to
CC screen for drugs to be used for cancer therapy, and the protein
CC itself may also be used to restore MTS function in a cell.
XX
XX Sequence 156 AA:
SQ

```

Query Match 81.8%; Score 121; DB 19; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 28 ALPNAFNSYGRPIQVMMGSAFYAEILLHGAEPCADPATLTRPVHDAAREGFIDTLV 87
DB 36 alpnafnsgyrrpdyvmmggsarvae11llhgaeppcadpatltrpvdaaregfldtlv 95
QY 88 VLRAGARLDVDRDAMGRPLVDLAEEIGHRDVARYLRAAAGTSGSNHARIDAAGPSDIP 147
DB 96 vlhragarldvdrdawgrlplvdlaeeighrdvarylraaagtrsgsnharidaaegpsdip 155
QY 148 D 148
DB 156 d 156

```

```

RESULT 15
AAW40524
ID AAW40524 standard; Protein; 156 AA.
XX
XX AAW40524;
AC
XX 15-JUL-1998 (first entry)
DT
XX
XX Human MTS1 protein.
DE
XX
XX MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
KW familial melanoma locus; MLM; predisposition.
XX
XX Homo sapiens.
OS
XX US5739027-A.
PN
XX 14-APR-1998.
PD
XX
XX 07-JUN-1995; 95US-0487033.
PF
XX
PR 07-JUN-1995; 95US-0487033.
PR 18-MAR-1994; 94US-0214582.
PR 18-MAR-1994; 94US-0215086.
PR 18-MAR-1994; 94US-0215087.
PR 14-APR-1994; 94US-0227369.
PR 01-JUN-1994; 94US-0251938.
PR 17-MAR-1995; 95WO-US03316.
XX
XX (MYRI-) MYRIAD GENETICS INC.
PA
XX
XX Kamb A;
PI
XX
XX WPI: 1998-250421/22.
DR N-PSDB; AAV11238.
XX
XX DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are
PT useful for the diagnosis of cancers related to MTS1E1-beta
PT mutation(s) and their treatment
XX
XX Disclosure; Column 63-64; 72pp; English.
XX
XX This sequence represents a human multiple tumour suppression protein,
CC MTS1. The MTS gene locus is also referred to as the familial melanoma
CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations
CC in MTS genes can be used in the diagnosis of predisposition to cancers,
CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
CC ovary, uterus, testis, kidney, stomach and rectum.
XX
XX Sequence 156 AA:
SQ

```

Query Match 81.8%; Score 121; DB 19; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 28 ALPNAFNSYGRPIQVMMGSAFYAEILLHGAEPCADPATLTRPVHDAAREGFIDTLV 87
DB 36 alpnafnsgyrrpdyvmmggsarvae11llhgaeppcadpatltrpvdaaregfldtlv 95
QY 88 VLRAGARLDVDRDAMGRPLVDLAEEIGHRDVARYLRAAAGTSGSNHARIDAAGPSDIP 147
DB 96 vlhragarldvdrdawgrlplvdlaeeighrdvarylraaagtrsgsnharidaaegpsdip 155
QY 148 D 148
DB 156 d 156

```

RESULT 16  
 AAW80524  
 ID AAW80524 standard; Protein; 156 AA.

```

XX AC AAW80524;
XX DT 03-FEB-1999 (first entry)
XX DE A human multiple tumour suppressor 1 (MTS1) protein.
XX KW Human; multiple tumour suppressor 1 gene; MTS1; cancer.
XX OS Homo sapiens.
XX PN US5843756-A.
XX PD 01-DEC-1998.
XX PF 28-JUL-1995; 95WO-0508735.
XX PR 28-JUL-1995; 95US-0508735.
XX PR 07-JUN-1995; 95US-0487033.
XX (MYRI-) MYRIAD GENETICS INC.
PI Jiang P, Kamb A, Stone S;
XX WPI: 1999-044585/04.
XX DR N-PSDB; AAV70583.
XX PT Mouse multiple tumour suppressor gene segment - useful for primer
XX design
XX PS Disclosure; Columns 65-66; 80pp; English.
XX CC The present sequence represents a human multiple tumour suppressor 1
XX CC (MTS1) protein. The sequence is homologous to the corresponding
XX CC murine gene. Primers designed from the gene can be used to design
XX CC primers to detect abnormalities i.e. polymorphisms which may
XX CC predispose towards malignancies such as melanoma, leukaemia,
XX CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
XX CC thyroid, pancreas, uterus and kidneys.
XX SQ Sequence 156 AA;

Query Match 81.8%; Score 121; DB 20; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAANSYGRPIQVMMGSAKYAEELLHGAEPCADPATLTTRPVHDAAREGFLDTLV 87
DB 36 alpnapnsygrtpiqvmmngsarvaeelllhgaepncadpatlttrpvhdaaregfltdtlv 95
QY 88 VLHRAGARLDVDRDAMGRLPVDLAEEELGHRDVARYLRAAGTGRGSNNHARIDAEGPSDIP 147
DB 96 vlhragarldvdrdagrllpvdlaeeelghrdvarylraaagtrgsnharidaaegpsdip 155
QY 148 D 148
DB 156 d 156

RESULT 17
AAB15498
ID AAB15498 standard; Protein; 156 AA.
XX
AC AAB15498;
XX
DT 14-FEB-2001 (first entry)
XX
DE Human MTS1 protein.
XX
KW Cytostatic; human; multiple tumour suppressor 1; MTS1; diagnostic;
XX cancer; gene therapy; protein replacement therapy.
XX

```

```

OS OS Homo sapiens.
XX PN US6090578-A.
XX PD 18-JUL-2000.
XX PF 08-DEC-1997; 97US-0986515.
XX PR 07-JUN-1995; 95US-0480810.
XX PR 18-MAR-1994; 94US-0214582.
XX PR 18-MAR-1994; 94US-0215086.
XX PR 18-MAR-1994; 94US-0215087.
XX PR 14-APR-1994; 94US-0227369.
XX PR 01-JUN-1994; 94US-0251938.
XX PR 17-MAR-1995; 95WO-US03316.
XX (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
XX WPI: 2000-514036/46.
XX DR N-PSDB; AAA95633.
XX PT Novel protein composition useful in protein replacement therapy for
XX PT diagnosing and treating cancer comprises a specific weight percent of
XX PT human multiple tumour suppressor 1 polypeptide -
XX PS Claim 4; Column 63-64; 72pp; English.
XX CC This sequence represents the human multiple tumour suppressor 1 (MTS1) in
XX CC amino acid sequence. The protein has a cytosolic activity and is used in
XX CC protein replacement therapy. MTS1 is useful in diagnosing human cancers
XX CC such as (ocular) melanoma, leukemia, astrocytoma, glioblastoma, lymphoma,
XX CC glioma, Hodgkin's lymphoma, multiple myeloma, sarcoma, myosarcoma,
XX CC cholangiocarcinoma, squamous cell carcinoma, CLL, and cancers of
XX CC pancreas, breast, stomach, brain, prostate, bladder, thyroid, ovary,
XX CC uterus, testis, kidney, colon and rectum. The MTS1 gene and protein is
XX CC useful in gene therapy, protein replacement therapy and protein mimetic
XX CC studies.
XX SQ Sequence 156 AA;

Query Match 81.8%; Score 121; DB 21; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAANSYGRPIQVMMGSAKYAEELLHGAEPCADPATLTTRPVHDAAREGFLDTLV 87
DB 36 alpnapnsygrtpiqvmmngsarvaeelllhgaepncadpatlttrpvhdaaregfltdtlv 95
QY 88 VLHRAGARLDVDRDAMGRLPVDLAEEELGHRDVARYLRAAGTGRGSNNHARIDAEGPSDIP 147
DB 96 vlhragarldvdrdagrllpvdlaeeelghrdvarylraaagtrgsnharidaaegpsdip 155
QY 148 D 148
DB 156 d 156

RESULT 18
AAV97524
ID AAV97524 standard; Protein; 156 AA.
XX
AC AAV97524;
XX
DT 15-JAN-2001 (first entry)
XX
DE Human p16 protein sequence.
XX
KW Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;
XX adenovirus E4 protein; neoplasia; p16 protein.
XX

```

```

OS Homo sapiens.
XX
PN WO200052184-A1.
XX
PD 08-SEP-2000.
XX
PF 01-MAR-2000; 2000WO-US05350.
XX
PR 01-MAR-1999; 99US-0122974.
PR 08-APR-1999; 99US-0128271.
PR 09-APR-1999; 99US-0128515.
XX
PA (CELL-) CELL GENESYS INC.
PA (MITO-) MITOTIX INC.
XX
PI Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;
DR WPI: 2000-587315/55.
DR N-PSDB; AAA90921.
XX
XX
XX Protein and nucleic acid compositions for preventing and treating
P1 neoplasias (particularly cancer), comprises a novel chimeric cyclin
PT dependent kinase inhibitor and adenovirus E4 protein
XX
PS Example 1; Page 123; 126pp; English.
XX
XX This sequence represents the human p16 protein.
CC The invention relates to a protein composition comprising a novel
CC purified chimeric cyclin dependent kinase inhibitor (CDKi) and a
CC purified adenovirus E4 protein. The compositions comprising the protein,
CC or the DNA encoding it are useful for treating neoplasias in animals. The
CC compositions also find use in assays to eliminate a specific
CC subpopulation of cultured cells, to determine the susceptibility of
CC neoplastic cells to treatment with the compositions and also in assays to
CC synchronise cell growth in cultured cells.
XX
SQ Sequence 156 AA;

```

Query Match 81.8%; Score 121; DB 21; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 28 ALPNAPNSYGRPRPIQVMMGSAVAEELLHGAEPCADPATLTRPVHDAAREGFLDTLV 87
DB 36 alpnapnsygrprpqymmgasrvaellllhgaeppcadpatltrpvdaaregfldtlv 95
QY 88 VLAHAGARLDVARDWGRPLPYDLAEELGHRDVARYLRAAAGTGRGNSNHARIDAEGPSDIP 147
D 96 vlhagarlvdardwgrlpydlaeelghrdvarylraaagtgtrgnsnharidaaegpsdip 155
QY 148 D 148
DB 156 d 156

```

RESULT 19  
 ID AAY96053 standard; Protein; 156 AA.  
 AC AAY96053;  
 XX  
 DT 05-DEC-2000 (first entry)  
 XX  
 DE Human cyclin dependent kinase inhibitor p16.  
 XX  
 KW Cyclin dependent kinase inhibitor; CDKi; INK4; human; p16;  
 KW smooth muscle cell; restenosis; vasotrophic; antiproliferative;  
 KW gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200052159-A1.

```

XX
PD 08-SEP-2000.
XX
PF 28-FEB-2000; 2000WO-US04971.
XX
PR 01-MAR-1999; 99US-0122974.
PR 05-NOV-1999; 99US-0163682.
PR 09-DEC-1999; 99US-0457368.
XX
PA (CELL-) CELL GENESYS INC.
PA (MITO-) MITOTIX INC.
XX
PI McArthur J, Gyuris J, Finer M;
DR WPI: 2000-594183/56.
DR N-PSDB; AAA50500.
XX
XX
XX Novel recombinant lentivirus for inhibiting proliferation of smooth
PT muscle cells in e.g. restenosis, its replication deficient and comprises
PT a transgene encoding a cyclin dependent kinase inhibitor
XX
PS Example 1; Page 121; 126pp; English.
XX
XX The present sequence is that of human p16, a cyclin dependent
CC kinase inhibitor (CDKi) that inhibits smooth muscle cell
CC proliferation. A claimed method for inhibiting smooth muscle cell
CC hyperproliferation involves transducing smooth muscle cells with a
CC replication-deficient recombinant adenovirus that lacks a functional
CC E1 region and a functional E4 region, and comprises a transgene
CC encoding a CDKi. The CDKi is selected from an INK4 family protein
CC such as human p16, a CIP/KIP family protein such as p27, active
CC fragments of these, or fusion proteins comprising (active fragments
CC of) an INK4 family protein and a CIP/KIP family protein (see AAY96046
CC and AAY96049). The method is used to inhibit mammalian smooth muscle
CC cell hyperproliferation induced by injury caused by angioplasty,
CC stent placement or vein occlusion. It is useful for treating
CC vascular pathologies, e.g. restenosis. Also claimed are recombinant
CC lentiviruses encoding CDKis.
XX
SQ Sequence 156 AA;

```

Query Match 81.8%; Score 121; DB 21; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 28 ALPNAPNSYGRPRPIQVMMGSAVAEELLHGAEPCADPATLTRPVHDAAREGFLDTLV 87
DB 36 alpnapnsygrprpqymmgasrvaellllhgaeppcadpatltrpvdaaregfldtlv 95
QY 88 VLAHAGARLDVARDWGRPLPYDLAEELGHRDVARYLRAAAGTGRGNSNHARIDAEGPSDIP 147
D 96 vlhagarlvdardwgrlpydlaeelghrdvarylraaagtgtrgnsnharidaaegpsdip 155
QY 148 D 148
DB 156 d 156

```

RESULT 20  
 ID AAY96067 standard; Protein; 156 AA.  
 AC AAY96067;  
 XX  
 DT 05-DEC-2000 (first entry)  
 XX  
 DE Human cyclin dependent kinase inhibitor p16.  
 XX  
 KW Cyclin dependent kinase inhibitor; CDKi; INK4; human; p16;  
 KW angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;  
 KW endometriosis; psoriasis; vascular retinopathy; cytostatic;  
 KW antiarthritic; antirheumatic; gynaecological; antipsoriatic;

KW antiproliferative; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200052158-A1.  
 XX  
 PD 08-SEP-2000.  
 XX  
 PE 28-FEB-2000; 2000MO-US04970.  
 XX  
 PR 01-MAR-1999; 99US-0122974.  
 PR 05-NOV-1999; 99US-0163682.  
 PR 09-DEC-1999; 99US-0457646.  
 XX  
 PA (CELL-) CELL GENESYS INC.  
 PA (MITO-) MITOTIX INC.  
 PI Patel S, McArthur J, Gyuris J;  
 PI  
 PI WPI: 2000-565501/52.  
 PI N-PSDB; AAA50520.

PT Inhibiting angiogenesis and treating angiogenesis-associated  
 PT conditions, e.g. neoplasia, psoriasis by transducing an endothelial  
 PT cell with a recombinant virus having a transgene encoding a cyclin  
 PT dependent kinase inhibitor -  
 XX  
 XX  
 PS Example 1; Page 129; 138pp; English.

CC The present sequence is that of human p16, a cyclin dependent  
 CC kinase inhibitor (CDK1) that inhibits angiogenesis. A claimed  
 CC method for inhibiting angiogenesis involves transducing an  
 CC epithelial cell with a transgene encoding (internally, a  
 CC secreted) CDK1. The delivery system for the transgene may be a  
 CC liposome or a recombinant virus. The CDK1 is preferably a protein  
 CC of the CIP/KIP family such as p27, a protein of the INK4 family  
 CC such as p16, active fragments of these proteins, or a fusion of 2  
 CC CDK1 proteins such as p27 and p16 (see AAY96068-80). The method is  
 CC useful in treating conditions associated with angiogenesis, e.g.  
 CC neoplasia, rheumatoid arthritis, endometriosis, psoriasis and  
 CC vascular retinopathy (claimed). Alternatively, the transgene is  
 CC delivered to an auxiliary cell, and is expressed by that cell such  
 CC that the CDK1 is released into the blood and contacts the target  
 CC epithelial cell.  
 XX  
 XX  
 SQ Sequence 156 AA;

Query Match 81.8%; Score 121; DB 21; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAKVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLY 87  
 Db |  
 Db 36 alpnapnsygrpipyvmungsarvaeellllhgaepncadpatltrpvdaaregfltdltv 95  
 QY 88 VLHRAARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTGTGSNHAARIDAAGSPSDIP 147  
 Db |  
 Db 96 vlhragarldvrdawgrylpvdlaeelghrdvarylraaagtgtrgsnharidaaegpsdip 155  
 QY 148 D 148  
 Db |  
 Db 156 d 156

RESULT 21  
 AAY92921  
 ID AAY92921 standard; Protein; 156 AA.  
 XX  
 AC AAY92921;  
 XX  
 DT 11-OCT-2000 (first entry)  
 XX

DE Human multiple tumour suppressor 1 protein.  
 XX  
 XX Variant; human; multiple tumour suppressor; MTS; mutation; melanoma;  
 KW cancer; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6037462-A.  
 XX  
 PD 14-MAR-2000.  
 XX  
 PE 22-JUL-1998; 98US-0120130.  
 XX  
 PR 07-JUN-1995; 95US-0480810.  
 PR 18-MAR-1994; 94US-0214582.  
 PR 18-MAR-1994; 94US-0215086.  
 PR 18-MAR-1994; 94US-0215087.  
 PR 14-APR-1994; 94US-0227369.  
 PR 01-JUN-1994; 94US-0251938.  
 PR 17-MAR-1995; 95MO-US03316.  
 XX  
 PA (MTR1-) MTR1AD GENETICS INC.  
 PI  
 PI Kamb A;  
 PI  
 PI WPI: 2000-269915/23.  
 PI N-PSDB; AAA11165.

PT New mutants of the human multiple tumor suppressor gene, useful as  
 PT diagnostic markers of cancer, contain specific base alterations or  
 PT deletions -  
 XX  
 XX  
 PS Disclosure; Column 61-62; 72pp; English.

CC The invention relates to variants (AAA11196-A11206) of the human  
 CC multiple tumour suppressor 1 (MTS1) protein of which this sequence  
 CC represents the wild type sequence. The variants have the following  
 CC changes relative to the wild type coding sequence: A at any of positions  
 CC 265, 442, 330 and 329; T at any of positions 172, 238, 341 and 148 and  
 CC deletions of nucleotides 290-294, 172-179 or 128-129. The variants are  
 CC somatic mutations of MTS1, indicative of predisposition to melanoma and  
 CC many other cancers, so detecting them is useful for diagnosis. Prognosis  
 CC and monitoring of cancer (including prenatal analysis). Cells and  
 CC animals that express the variants are useful as model systems for  
 CC identifying potential anticancer agents.  
 XX  
 XX  
 SQ Sequence 156 AA;

Query Match 81.8%; Score 121; DB 21; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAKVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLY 87  
 Db |  
 Db 36 alpnapnsygrpipyvmungsarvaeellllhgaepncadpatltrpvdaaregfltdltv 95  
 QY 88 VLHRAARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTGTGSNHAARIDAAGSPSDIP 147  
 Db |  
 Db 96 vlhragarldvrdawgrylpvdlaeelghrdvarylraaagtgtrgsnharidaaegpsdip 155  
 QY 148 D 148  
 Db |  
 Db 156 d 156

RESULT 22  
 AAY91102  
 ID AAY91102 standard; Protein; 156 AA.  
 XX  
 AC AAY91102;  
 XX  
 DT 12-SEP-2000 (first entry)  
 XX



QY 88 VLRAGARLDVDRDAMGRPLVDLAEEIGHRDVARYLRAAAGCTRGSHNRIDAEGPSDIP 147  
 |  
 Db 96 vlhragarldvdrdawgripvdlaeelghrdvarylraaagctrgshnaridaaegpsdip 155  
 QY 148 D 148  
 |  
 Db 156 d 156

## RESULT 24

AAV54902

ID AAV54902 standard; Protein: 156 AA.

XX AAV54902;

XX 11-FEB-2000 (first entry)

XX Human multiple tumour suppressor 1 protein sequence.

XX Multiple tumour suppressor: MTS2, human; diagnosis; Hodgkin's lymphoma;  
 cancer predisposition; melanoma; leukaemia; lymphoma; glioma; MTS1.

XX Homo sapiens.

XX US5994095-A.

XX 30-NOV-1999.

XX 07-JUN-1995; 95US-0486047.

XX 18-MAR-1994; 94US-0214582.

XX 18-MAR-1994; 94US-0215086.

XX 18-MAR-1994; 94US-0215087.

XX 14-APR-1994; 94US-0227369.

XX 01-JUN-1994; 94US-0251938.

XX 17-MAR-1995; 95WO-US03316.

XX (MYRI-) MYRIAD GENETICS INC.

XX Kamb A;

XX WPI: 2000-038259/03.

XX N-PSDB: AA239974.

XX Multiple tumour suppressor cDNA, useful for diagnosing or determining a

XX predisposition to cancer -

XX Disclosure: Column 61-62; 72pp; English.

XX This sequence represents the human multiple tumour suppressor 1 (MTS1)

XX protein. The invention relates to the human MTS2 DNA and protein

XX sequences. The DNA sequences are useful for diagnosing or determining a

XX predisposition to cancers e.g. melanoma, leukaemia, lymphoma, glioma,

XX Hodgkin's lymphoma and cancers of the pancreas, breast, thyroid, ovary,

XX kidney, uterus and stomach.

XX Sequence 156 AA;

XX

QY 148 D 148

Db 156 d 156

## RESULT 25

AAU02122

ID AAU02122 standard; Protein: 156 AA.

XX AAU02122;

XX 29-AUG-2001 (first entry)

XX Human multiple tumour suppressor MTS1, amino acid sequence.

XX Human: multiple tumour suppressor: MTS1; MTS2; therapeutic; diagnostic;  
 cancer; gene therapy; melanoma; leukaemia; astrocytoma; glioblastoma;

XX lymphoma; glioma; Hodgkin's lymphoma; chronic lymphatic leukaemia.

XX Homo sapiens.

XX US6210949-B1.

XX 03-APR-2001.

XX 30-NOV-1998; 98US-0201139.

XX 28-JUL-1995; 95US-0508735.

XX 17-MAR-1995; 95WO-US03316.

XX 07-JUN-1995; 95US-0487033.

XX (MYRI-) MYRIAD GENETICS INC.

XX Stone S, Jiang P, Kamb A;

XX WPI: 2001-280859/29.

XX N-PSDB: AA502564.

XX New mouse multiple tumour suppressor gene, useful for diagnosing or

XX prognosing human cancer or as gene therapy for treating cancer,

XX particularly melanoma, leukaemia, astrocytoma, lymphoma or cancers of

XX the pancreas or breast -

XX Disclosure: Fig 19; 80pp; English.

XX The sequence represents the amino acid sequence of human multiple tumour

XX suppressor MTS1. The MTS genes, and expression products, are useful for

XX treating, diagnosing or prognosing human cancer. In particular, the MTS

XX gene is useful for diagnosing a predisposition to or as a gene therapy

XX for melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,

XX Hodgkin's lymphoma, chronic lymphatic leukaemia (CLL), or cancers of the

XX pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach or

XX rectum. The gene may be used in both cancerous and pre-cancerous cells.

XX Sequence 156 AA;

XX

QY 28 ALPNAPNSYGRPIQVMMGSAKYAEILLHGAEPNCADPATLTRPVHDAAREGFLDTLY 87

Db 36 alpnapnsygrripqymmgasrvaellllhgaepncadpatltrpvhaaregfltdtlv 95

QY 88 VLRAGARLDVDRDAMGRPLVDLAEEIGHRDVARYLRAAAGCTRGSHNRIDAEGPSDIP 147

Db 96 vlhragarldvdrdawgripvdlaeelghrdvarylraaagctrgshnaridaaegpsdip 155

QY 148 D 148

Db 156 d 156

```

RESULT 26
ID AAE01002 standard; Protein; 156 AA.
XX
XX AAE01002;
XX
XX 04-JUL-2001 (first entry)
XX
XX Human multiple tumor suppressor 1 (MTS1) protein.
XX
XX Human; multiple tumor suppressor; MTS1; cytosolic; somatic mutation;
XX germ line mutation; gene therapy; melanoma; leukaemia; astrocytoma; CLL;
XX glioblastoma; lymphoma; glioma; Hodgkin's lymphoma; cancer; rectum;
XX pancreas; breast; thyroid; ovary; uterus; testis; kidney; stomach;
XX chromosome 9p21.
XX
XX Homo sapiens.
XX
XX US6218146-B1.
XX
XX 17-APR-2001.
XX
XX 22-JUL-1998; 98US-0120131.
XX
XX 07-JUN-1995; 95US-0486047.
XX 18-MAR-1994; 94US-0214582.
XX 18-MAR-1994; 94US-0215086.
XX 18-MAR-1994; 94US-0215087.
XX 14-APR-1994; 94US-0227369.
XX 01-JUN-1994; 94US-0251938.
XX 17-MAR-1995; 95WO-0503316.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Kamb A;
XX
XX WPI: 2001-289831/30.
XX N-PSDB; AAD04692, AAD04693, AAD04694, AAD04724, AAD04727, AAD04734,
XX AAD04735.
XX
XX Novel multiple tumor suppressor proteins useful for diagnosis and
XX prognosis of human cancer and for screening drugs for cancer treatment
XX
XX
XX Example 9; Column 63-64; 71pp; English.
XX
XX The invention relates to somatic and germ line mutations in the
XX multiple tumor suppressor (MTS) gene in human cancer. The invention
XX also relates to therapy of human cancer which have a mutation in the
XX MTS gene, including gene therapy, protein replacement therapy, and
XX protein mimetics. The MTS sequences are useful for diagnosing
XX predisposition to human cancer or for diagnosing and prognosing
XX human cancers such as melanoma, leukaemia, astrocytoma, glioblastoma,
XX lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers of pancreas,
XX breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.
XX They are also used for screening drugs for cancer treatment.
XX The present sequence is human MTS1 protein which is encoded on
XX chromosome 9p21.
XX
XX Sequence 156 AA;

```

```

Query Match 81.8%; Score 121; DB 22; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 28 ALPNAPNSYGRPIQVMMGSAFYAEILLHGAEPCADPATLTRPVHDAAREGFLDTLY 87
DB 36 alpnapnsygrripqymmmgsarvaeilllhgaepncadpatltrpvhaaregfltdltv 95
OY 88 VLHRAGARLDVDAWGRLPVDLAEEELGHRDVARYLRAAAGTSGSHARIDAAGPSDIP 147
DB 96 vlhragarldvrdawgrlpvdlaeelghrdvarylraaagtrsgsharidaaegpsdip 155

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```

RESULT 27
ID AAB67334 standard; protein; 156 AA.
XX
XX AAB67334;
XX
XX 23-APR-2001 (first entry)
XX
XX Protein encoded by multiple tumour suppressor open reading frame #2.
XX
XX Human; multiple tumour suppressor; MTS; cancer; gene therapy.
XX
XX Homo sapiens.
XX
XX US6180776-B1.
XX
XX 30-JAN-2001.
XX
XX 22-JUL-1998; 98US-0120129.
XX
XX 07-JUN-1995; 95US-0486047.
XX 18-MAR-1994; 94US-0214582.
XX 18-MAR-1994; 94US-0215086.
XX 18-MAR-1994; 94US-0215087.
XX 01-JUN-1994; 94US-0251938.
XX 17-MAR-1995; 95WO-0503316.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Kamb A;
XX
XX WPI: 2001-158668/16.
XX
XX Novel multiple tumor suppressor gene useful for diagnosing, prognosing
XX and treating cancers, such as melanoma, leukemia, glioblastoma and
XX Hodgkin's lymphoma -
XX
XX Disclosure; Column 63; 71pp; English.
XX
XX The present invention relates to human multiple tumor suppressor-2
XX (MTS2) gene. The invention is useful for diagnosing, prognosing and
XX treating cancers. It is also useful for screening drugs for cancer
XX therapy and gene therapy.
XX
XX Sequence 156 AA;

```

```

XX AAB36890;
AC 23-FEB-2001 (first entry)
XX
XX Human Multiple Tumour Suppressor 1 protein.
DE
XX MTS; Multiple Tumour Suppressor; cancer; antibody.
XX
XX Homo sapiens.
XX
XX US6140473-A.
XX
XX 31-OCT-2000.
XX
XX 22-JUL-1998; 98US-0120128.
XX
XX 07-JUN-1995; 95US-0486047.
XX 18-MAR-1994; 94US-0214582.
XX 18-MAR-1994; 94US-0215086.
XX 18-MAR-1994; 94US-0215087.
XX 14-APR-1994; 94US-0227369.
XX 01-JUN-1994; 94US-0251938.
XX 17-MAR-1995; 95WO-US03316.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Kamb A;
XX
XX WPI; 2001-014867/02.
XX N-PSDB; AAC83071.
XX
XX New multiple tumor suppressor 2-specific antibodies useful for
XX detecting differences in the absence of the peptides or mutant gene
XX products, or for screening tissues -
XX
XX Claim 1; Column 63; 71pp; English.
XX
XX The present invention relates to an antibody or its fragment that
XX specifically binds to a human multiple tumour suppressor (MTS). The
XX invention is useful for detecting differences in the absence of MTS
XX peptides; to screen a tissue or to detect mutant MTS gene products.
XX The antibodies will immunoprecipitate MTS proteins from solution as
XX well as react with MTS protein on Western or immunoblots of
XX polyacrylamide gels.
XX
XX Sequence 156 AA;
SQ
Query Match 81.8%; Score 121; DB 22; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28 ALPNAPNSYGRPIOVMMGSAARVAEILLHGAEPCADPATLTPRVHDAAREGFLDTLV 87
DB 36 alpnapnsygrripqymmmgsarvaeilllhgaepncadpatltprvhdaaregfldtlv 95
QY 88 VLHRAGARLDVDAWGRLPVDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 147
DB 96 vlhrtagarldvrdawgrlpvdlaeelghrdvarylraaagtrsgsnharidaegpsdip 155
QY 148 D 148
DB 156 d 156
RESULT 29
AA97522
ID AA97522 standard; Protein; 228 AA.
XX
XX AA97522;
XX
XX 15-JAN-2001 (first entry)
XX

```

```

XX Human W9 protein sequence.
DE
XX Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;
XX adenovirus E4 protein; neoplasia; W9 protein.
XX
XX Homo sapiens.
XX
XX WO200052184-A1.
XX
XX 08-SEP-2000.
XX
XX 01-MAR-2000; 2000WO-US05350.
XX
XX 01-MAR-1999; 99US-0122974.
XX 08-APR-1999; 99US-0128271.
XX 09-APR-1999; 99US-0128515.
XX
XX (CELL-) CELL GENESYS INC.
XX (MITO-) MITOTIX INC.
XX
XX Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;
XX
XX WPI; 2000-587315/55.
XX N-PSDB; AAA90919.
XX
XX Protein and nucleic acid compositions for preventing and treating
XX neoplasias (particularly cancer), comprises a novel chimeric cyclin
XX dependent kinase inhibitor and adenovirus E4 protein -
XX
XX Example 1; Fig 2b; 126pp; English.
XX
XX This sequence represents the human W9 protein.
XX The invention relates to a protein composition comprising a novel
XX purified chimeric cyclin dependent kinase inhibitor (CDK1) and a
XX or the DNA encoding it are useful for treating neoplasias in animals. The
XX compositions also find use in assays to eliminate a specific
XX subpopulation of cultured cells, to determine the susceptibility of
XX neoplastic cells to treatment with the compositions and also in assays to
XX synchronise cell growth in cultured cells.
XX
XX Sequence 228 AA;
SQ
Query Match 81.8%; Score 121; DB 21; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.2e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28 ALPNAPNSYGRPIOVMMGSAARVAEILLHGAEPCADPATLTPRVHDAAREGFLDTLV 87
DB 108 alpnapnsygrripqymmmgsarvaeilllhgaepncadpatltprvhdaaregfldtlv 167
QY 88 VLHRAGARLDVDAWGRLPVDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 147
DB 168 vlhrtagarldvrdawgrlpvdlaeelghrdvarylraaagtrsgsnharidaegpsdip 227
QY 148 D 148
DB 228 d 228
RESULT 30
AA96051
ID AA96051 standard; Protein; 228 AA.
XX
XX AA96051;
XX
XX 05-DEC-2000 (first entry)
XX
XX Antiproliferative truncated p27-p16 fusion protein W9.
XX
XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; p27; INK4;
XX

```



KW p16; human; smooth muscle cell; hyperproliferation; restenosis;  
KW vasotrophic; antiproliferative; gene therapy; mutant; mutein.  
OS Homo sapiens.  
XX Synthetic.  
FH Key  
FT Protein  
FT Protein  
XX /label= p16  
XX /label= p16  
PN MOZ00052159-A1.  
PD 08-SEP-2000.  
XX 28-FEB-2000; 2000WO-USO4971.  
PF 01-MAR-1999; 99US-0122974.  
XX 05-NOV-1999; 99US-0163682.  
PR 09-DEC-1999; 99US-0457568.  
XX (CELL-) CELL GENESYS INC.  
PA (MITO-) MITOTIX INC.  
PI McArthur J, Gyuris J, Finer M;  
XX WPI: 2000-594183/56.  
DR N-PSDB: AAA50498.  
XX Novel recombinant lentivirus for inhibiting proliferation of smooth  
PT muscle cells in e.g. restenosis, is replication deficient and comprises  
PI a transgene encoding a cyclin dependent kinase inhibitor .  
XX  
PS Example 1; Page 118-119; 126pp; English.  
XX  
CC The present sequence is that of W9 fusion protein comprising a  
CC truncated human p27 protein (see AAY96048) in which only the cyclin  
CC dependent kinase inhibitor (CDK1) domain is retained, and human p16  
CC protein (see AAY96053), with no (GLY4Ser)3 hinge. A claimed method  
CC for inhibiting smooth muscle cell hyperproliferation involves  
CC transducing smooth muscle cells with a replication-deficient  
CC recombinant adenovirus that lacks functional E1 and E4 regions, and  
CC comprises a transgene encoding a CDK1. The CDK1 is selected from  
CC an INK4 family protein such as human p16, a CIP/KIP family protein  
CC such as p27, active fragments of these, or fusion proteins  
CC comprising (active fragments of) an INK4 family protein and a  
CC CIP/KIP family protein (see AAY96046 and AAY96049). A fusion protein  
CC comprising W9 is specifically claimed. The method is used to  
CC inhibit mammalian smooth muscle cell hyperproliferation induced  
CC by injury caused by angioplasty, stent placement or vein  
CC engraftment. It is useful for treating vascular pathologies e.g.,  
CC restenosis. Also claimed are recombinant lentiviruses encoding  
CC CDKis. Use of truncated p27 was designed to increase the protein's  
CC half-life and to eliminate potential phosphorylation sites involved  
CC in the negative regulation of CDK1 activity. The p27-p16 fusion  
CC proteins interact with the CDK4/cyclinD, CDK2/cyclina and  
CC CDK2/cycline complexes and inhibit cell cycle progression at  
CC multiple points.  
XX  
XX Sequence 228 AA;

Query Match	81.8%;	Score 121;	DB 21;	Length 228;
Best Local Similarity	100.0%;	Pred. No.	2.2e-108;	
Matches 121;	Conservative	0;	Mismatches	0;
		Indels	0;	Gaps

OY 28 ALPAPNSYGRBPIDVMAMGARSAREVELLILHGAEFNCADPATLRPVHDAAREGLDTLV 87  
db 108 alpnapnsygrripdyvmmgasrvaelllllhgaepncedpatltprvydaaregfditlv 167  
OY VLRAGRLDVNDAMGRLEPYDLAELGHBDVARIRAAAGGTSGNHAIDAEGPSDIP 147  
|||||

Db	168	vlnhagarltdvrdawgrlpvplaeelghrcvdrayl1raaagstgsmnaridaegpsdip	228
Qy	148	D 148	
Db	228	d 228	
RESULT 31			
AAy96078	ID	AAy96078 standard; Protein; 228 AA.	
AAy96078;	AC		
05-DEC-2000	DT	(first entry)	
Angiogenesis inhibitor p27(25-93)-p16 fusion W9.	XX		
Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; human; p27; angiogenesis; inhibitor; neoplasia; rheumatoid arthritis; endometriosis; psoriasis; vascular retinopathy; cytostatic; antiarthritic; antirheumatic; gynaecological; antipsoriatic; antiproliferative; gene therapy; mutant; mutein.	XX		
Homo sapiens.	XX		
Synthetic.	OS		
Key	FM	Location/Qualifiers	
Protein	FT	1..71	
Protein	FT	/label= p27(25-93)	
Protein	FT	84..228	
	FT	/label= p16	
WO200052158-A1.	PN		
08-SEP-2000.	XX		
28-FEB-2000; 2000WO-US04970.	PD		
01-MAR-1999; 99US-0122974.	PF		
05-NOV-1999; 99US-0163682.	PR		
09-DEC-1999; 99US-0457646.	PR		
(CELL-) CELL GENESYS INC.	PA		
(MITO-) MITOTIX INC.	PA		
Patel S, McArthur J, Gyuris J;	PI		
WPI; 2000-565501/52.	DR		
N-PSDB; AAA50533.	DR		
Inhibiting angiogenesis and treating angiogenesis-associated conditions, e.g. neoplasia, psoriasis by transducing an endothelial cell with a recombinant virus having a transgene encoding a cyclin dependent kinase inhibitor	PT		
Example 1; Page 126-127; 138pp; English.	PS		
The present sequence is that of fusion protein W9 comprising an N-terminal truncated human p27 protein (see AAy96075) in which only the cell dependent kinase inhibitory (CDK1) domain was retained, and a human p16 protein (see AAy96067). This version of W9 differs from that of AAy96076 by the lack of a haemagglutinin tag. A claimed method for inhibiting angiogenesis involves transducing an epithelial cell with a transgene encoding a CDK1. The transgene delivery system is a liposome or a recombinant virus. The CDK1 is a protein of the CIP/KIP family such as p27, a protein of the INK family such as p16, active fragments of these (e.g. amino acids 25-93 or 12-178 of human p27), or a fusion protein comprising 2 CDK1 proteins such as (truncated) p27 and p16 (see AAy96068-80). A method in which the CDK1 is W9 is specifically claimed. The method is used to treat conditions associated with angiogenesis, e.g. neoplasia, rheumatoid arthritis, endometriosis, psoriasis and vascular retinopathy (claimed). Alternatively, the transgene is			

CC delivered to an auxiliary cell, and is expressed by that cell such  
 CC that the CDK1 is released into the blood and contacts the target  
 CC epithelial cell. Use of truncated p27 was designed to increase the  
 CC protein's half-life and to eliminate potential phosphorylation sites  
 CC involved in the negative regulation of CDK1 activity.

XX Sequence 228 AA:

Query Match 81.8%; Score 121; DB 21; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 ALPNAPNSYGRPRIOVMNGSARVAELLHGAEPNCADPATLTRPVHDAREGFLDTLY 87  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 108 alpnapnsygrprigymmgasrvaellllngaepncadpaltlrpvdaaregfltdly 167  
 OY 88 VLHRRAGARLDVRDAMGRPLVDLAEEELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIP 147  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 168 vlhrragardvrdawgrlvpdlaaeelghrdvarylraaagtrsgsnharidaaegpsdip 227

148 D 148  
 |  
 DB 228 d 228

# RESULT 32

AAW95105  
 ID AAW95105 standard; Protein: 237 AA.

XX AAW95105;

XX 25-MAY-1999 (first entry)

DE Truncated p27/p16 fusion protein.

XX Cyclin-dependent kinase; CDK; cyclin complex; inhibitory; restenosis;  
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;  
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;  
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;  
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;  
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;  
 KW tachycardia; human; p27; p16; truncated.

XX Homo sapiens.

XX MO9906540-A2.

XX 11-FEB-1999.

XX 29-JUL-1998; 98MO-US15759.

XX 29-JUL-1997; 97US-0902572.

XX (MITO-) MITOTIX INC.

XX Beach DH, Gyuris J, Lamphere L;

XX WPI; 1999-153770/13.

XX N-PSDB; AAX26233.

PT Fusion and chimaeric proteins including cyclin-dependent kinase  
 PT binding motif - used for regulation of cell proliferation and  
 PT differentiation, for treatment of, e.g. vascular injury, cancers,  
 PT fibrosis and neurodegeneration

XX Claim 63; Page 85; 88pp; English.

XX The invention relates to novel inhibitors of cyclin-dependent kinases  
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant  
 CC transfection system (A) that comprises: (i) first gene construct  
 CC comprising a sequence encoding an inhibitory polypeptide containing at  
 CC least one CDK-binding motif for binding and inhibiting activity of a

CC CDK, linked to a transcription regulator functional in eukaryotic cells;  
 CC (ii) second gene construct comprising a sequence encoding a polypeptide  
 CC that promotes endothelialisation, and (iii) a gene delivery composition  
 CC for delivering the GCs to a cell for transfection. Also provided are  
 CC nucleic acids encoding a fusion protein (FP) containing: (i) a  
 CC therapeutic polypeptide sequence (TP) from an intracellular protein that  
 CC alters a cellular process when FP enters the cell, and (ii) a  
 CC transcellular polypeptide sequence (TCP) that promotes transcytosis of  
 CC FP. The FP consists of at least one CDK-binding motif and a TCP. See  
 CC AAX26220 for detailed uses of the recombinant transfection system. The  
 CC present sequence represents a human truncated p27/p16 fusion protein.

XX Sequence 237 AA:

Query Match 81.8%; Score 121; DB 20; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 ALPNAPNSYGRPRIOVMNGSARVAELLHGAEPNCADPATLTRPVHDAREGFLDTLY 87  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 117 alpnapnsygrprigymmgasrvaellllngaepncadpaltlrpvdaaregfltdly 176  
 OY 88 VLHRRAGARLDVRDAMGRPLVDLAEEELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIP 147  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 177 vlhrragardvrdawgrlvpdlaaeelghrdvarylraaagtrsgsnharidaaegpsdip 236

OY 148 D 148  
 |  
 DB 237 d 237

# RESULT 33

AAW97534  
 ID AAW97534 standard; Protein: 237 AA.

XX AAW97534;

XX 15-JAN-2001 (first entry)

DE Human W9 protein sequence.

XX Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;  
 KW adenovirus E4 protein; neoplasia; W9 protein.

XX Homo sapiens.

XX WO200052184-A1.

XX 08-SEP-2000.

XX 01-MAR-2000; 2000MO-US05350.

XX 01-MAR-1999; 99US-0122974.

XX 08-APR-1999; 99US-0128271.

XX 09-APR-1999; 99US-0128515.

XX (CELL-) CELL GENESYS INC.

XX (MITO-) MITOTIX INC.

XX Patel S, McArthur J, Gyuris J, Mendez MO, Flier M;

XX WPI; 2000-587315/55.

XX N-PSDB; AAA90931.

XX Protein and nucleic acid compositions for preventing and treating  
 PT neoplasias (particularly cancer), comprises a novel chimeric cyclin  
 PT dependent kinase inhibitor and adenovirus E4 protein -

XX Example 1; Page 119; 126pp; English.  
 CC This sequence represents the human W9 protein.  
 CC The invention relates to a protein composition comprising a novel

CC purified chimeric cyclin dependent kinase inhibitor (CDKi) and a  
 CC purified adenovirus E4 protein. The compositions comprising the protein,  
 CC or the DNA encoding it are useful for treating neoplasias in animals. The  
 CC compositions also find use in assays to eliminate a specific  
 CC sub-population of cultured cells, to determine the susceptibility of  
 CC neoplastic cells to treatment with the compositions and also in assays to  
 CC synchronise cell growth in cultured cells.

XX Sequence 237 AA:

Query Match 81.8%; Score 121; DB 21; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 ALPNAPNSYGRPIQVMMGSAVAEILLHGAEPCADPATLTRPVHDAAREGFLDTLV 87  
 DB 117 alpnaensygrripqymmgasrvaellllhgaepncadpatltrpvhdaaregfltdltv 176  
 OY 88 VLHRAGARLDVRDAMGRLPVDLAELGHRDVARYLRAAAGTGRGSNHARIDAAEGPSDIP 147  
 DB 177 vlhragarldvrdaawgrlpvdlaelghrdvarylraaagtrgsnharidaaegpsdip 236

OY 148 D 148  
 DB 237 d 237

RESULT 34

AA96049  
 ID AAY96049 standard; Protein; 237 AA.

XX AAY96049;  
 XX  
 DT 05-DEC-2000 (first entry)

DE Antiproliferative truncated p27-p16 fusion protein W9.

XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; p27; INK4;  
 KW p16; human; smooth muscle cell; hyperproliferation; restenosis;  
 KM vasotropic; antiproliferative; gene therapy; mutant; mutein.

XX  
 OS Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Peptide 1..11  
 FT /label= Haemagglutinin epitope  
 FT Protein 12..80  
 FT /label= p27(25-93)  
 FT 94..237  
 FT /label= p16

PN WO200052159-A1.

PD 08-SEP-2000.

PF 28-FEB-2000; 2000MO-US04971.

XX 01-MAR-1999; 99US-0122974.  
 PR 05-NOV-1999; 99US-0163682.  
 PR 09-DEC-1999; 99US-0457568.

XX  
 PA (CELL-) CELL GENESYS INC.  
 PA (MITO-) MITOTIX INC.

PI McArthur J, Gyuris J, Finer M;

DR WPI; 2000-594183/56.

XX N-PSDB; AAA50496.

XX Novel recombinant lentivirus for inhibiting proliferation of smooth  
 PT muscle cells in e.g. restenosis, is replication deficient and comprises

PT a transgene encoding a cyclin dependent kinase inhibitor -  
 XX  
 PS Example 1; Page 115-116; 126pp; English.

XX The present sequence is that of W9 fusion protein comprising a  
 CC hemagglutinin tag, a truncated human p27 protein (see AAY96048) in  
 CC which only the cyclin dependent kinase inhibitor (CDKi) domain is  
 CC retained, and human p16 protein (see AAY96053). A claimed method for  
 CC inhibiting smooth muscle cell hyperproliferation involves  
 CC transducing smooth muscle cells with a replication-deficient  
 CC recombinant adenovirus that lacks functional E1 and E4 regions, and  
 CC comprises a transgene encoding a CDKi. The CDKi is selected from  
 CC an INK4 family protein such as human p16, a CIP/KIP family protein  
 CC such as p27, active fragments of these, or fusion proteins  
 CC comprising (active fragments of) an INK4 family protein and a  
 CC CIP/KIP family protein (see AAY96046 and AAY96049). A fusion protein  
 CC comprising W9 is specifically claimed. The method is used to  
 CC inhibit mammalian smooth muscle cell hyperproliferation induced  
 CC by injury caused by angioplasty, stent placement or vein  
 CC engraftment. It is useful for treating vascular pathologies e.g.,  
 CC restenosis. Also claimed are recombinant lentiviruses encoding  
 CC CDKis. Use of truncated p27 was designed to increase the protein's  
 CC half-life and to eliminate potential phosphorylation sites involved  
 CC in the negative regulation of CDKi activity. The p27-p16 fusion  
 CC proteins interact with the CDK4/cyclinD, CDK2/cyclinA and  
 CC CDK2/cyclinE complexes and inhibit cell cycle progression at  
 CC multiple points.

XX Sequence 237 AA:

Query Match 81.8%; Score 121; DB 21; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 ALPNAPNSYGRPIQVMMGSAVAEILLHGAEPCADPATLTRPVHDAAREGFLDTLV 87  
 DB 117 alpnaensygrripqymmgasrvaellllhgaepncadpatltrpvhdaaregfltdltv 176  
 OY 88 VLHRAGARLDVRDAMGRLPVDLAELGHRDVARYLRAAAGTGRGSNHARIDAAEGPSDIP 147  
 DB 177 vlhragarldvrdaawgrlpvdlaelghrdvarylraaagtrgsnharidaaegpsdip 236

OY 148 D 148

DB 237 d 237

RESULT 35

AA96076  
 ID AAY96076 standard; Protein; 237 AA.

XX AAY96076;

DT 05-DEC-2000 (first entry)

DE Angiogenesis inhibitor p27(25-93)-p16 fusion W9.

XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; human; p27;  
 KW angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;  
 KW endometriosis; psoriasis; vascular retinopathy; cytostatic;  
 KW antiarthritic; antirheumatic; gynaecological; antiproliferative;  
 KW antiproliferative; gene therapy; mutant; mutein.

XX Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Peptide 1..11  
 FT /label= Haemagglutinin epitope  
 FT Protein 12..80  
 FT /label= p27(25-93)  
 FT 94..237  
 FT Protein

```

FT      /label= p16
XX
XX      WO20052158-A1.
XX
XX      08-SEP-2000.
XX
XX      28-FEB-2000; 2000WO-US04970.
XX
XX      01-MAR-1999; 99US-0122974.
XX      05-NOV-1999; 99US-0163682.
XX      09-DEC-1999; 99US-0457646.
XX
XX      (CELL-) CELL GENESYS INC.
XX      (MITO-) MITOTIX INC.
XX
XX      Patel S, McArthur J, Gyuris J;
XX      WPI: 2000-565501/52.
XX      N-PSDB; AAA50531.
XX
XX      Inhibiting angiogenesis and treating angiogenesis-associated
XX      conditions, e.g. neoplasia, psoriasis by transducing an endothelial
XX      cell with a recombinant virus having a transgene encoding a cyclin
XX      dependent kinase inhibitor
XX
XX      Example 1; Page 123-124; 138pp; English.
XX
XX      The present sequence is that of fusion protein W9 comprising an
XX      N-terminal haemagglutinin tag, a truncated human p27 protein (see
XX      AAY96075) in which only the cell dependent kinase inhibitory domain
XX      was retained, and a human p16 protein (see AAY96067). A claimed method
XX      for inhibiting angiogenesis involves transducing an epithelial cell
XX      with a transgene encoding a cyclin dependent kinase inhibitor (CDKi).
XX      The delivery system is a liposome or a recombinant virus. The CDKi
XX      is a protein of the Cip/Kip family such as p27, a protein of the
XX      INK4 family such as p16, active fragments of these (e.g. amino acids
XX      25-93 or 12-178 of human p27), or a fusion protein comprising 2
XX      CDKi proteins such as (truncated) p27 and p16 (see AAY96068-80). A
XX      method in which the CDKi is W9 is specifically claimed. The
XX      method is used to treat conditions associated with angiogenesis,
XX      e.g. neoplasia, rheumatoid arthritis, endometriosis, psoriasis and
XX      vascular retinopathy (claimed). Alternatively, the transgene is
XX      delivered to an auxiliary cell, and is expressed by that cell such
XX      that the CDKi is released into the blood and contacts the target
XX      epithelial cell. Use of truncated p27 was designed to increase the
XX      protein's half-life and to eliminate potential phosphorylation sites
XX      involved in the negative regulation of CDKi activity.
XX
XX      Sequence      237 AA:
XX
XX      Query Match      81.8%; Score 121; DB 21; Length 237;
XX      Best Local Similarity 100.0%; Pred. No. 2.3e-108;
XX      Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      28 ALPNAPNSYGRPRIOVMWMSARVAELLHGAEPNCADPATLTRPVHDAAREGFDLTV 87
XX      |||||||
XX      Db 117 alpnapnsygrprpqvmwmsarvaeellllhgaepncadpatltrpvhdaaregfldtlv 176
XX
XX      QY 88 VLHRAGARLDVDAWGRIPVDLAEEIGHRDVARYLRAAAGTSGSNHARIDAEGSPSDIP 147
XX      |||||||
XX      Db 177 vlhragarlvdvdaawgrlvpdlaeelghrdvarylraaagtlrsgsnharidaegpsdip 236
XX
XX      QY 148 D 148
XX      |
XX      Db 237 d 237
XX
XX      RESULT 36
XX      AAW95106
XX      ID AAW95106 standard; Protein; 252 AA.
XX      AC AAW95106;.

```

```

XX      25-MAY-1999 (first entry)
XX
XX      Truncated p27/p16 fusion protein.
XX
XX      Cyclin-dependent kinase; CDK; cyclin complex; inhibitory; restenosis;
XX      CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
XX      intracellular; transcellular; arteriosclerosis; vascular wound; repair; hair;
XX      smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
XX      cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
XX      tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
XX      tachycardia; human; p27; p16; truncated.
XX
XX      Homo sapiens.
XX
XX      WO906540-A2.
XX
XX      11-FEB-1999.
XX
XX      29-JUL-1998; 98WO-US15759.
XX
XX      29-JUL-1997; 97US-0902572.
XX
XX      (MITO-) MITOTIX INC.
XX
XX      Beach DH, Gyuris J, Lamphere L;
XX      WPI: 1999-153770/13.
XX      N-PSDB; AAX26234.
XX
XX      Fusion and chimaeric proteins including cyclin-dependent kinase
XX      binding motif - used for regulation of cell proliferation and
XX      differentiation, for treatment of, e.g. vascular injury, cancers,
XX      fibrosis and neurodegeneration
XX
XX      Claim 63; Page 85; 88pp; English.
XX
XX      The invention relates to novel inhibitors of cyclin-dependent kinases
XX      (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
XX      transfection system (A) that comprises: (i) first gene construct
XX      comprising a sequence encoding an inhibitory polypeptide containing at
XX      least one CDK-binding motif for binding and inhibiting activity of a
XX      CDK, linked to a transcription regulator functional in eukaryotic cells;
XX      (ii) second gene construct comprising a sequence encoding a polypeptide
XX      that promotes endothelialisation, and (iii) a gene delivery composition
XX      for delivering the gcs to a cell for transfection. Also provided are
XX      nucleic acids encoding a fusion protein (FP) containing: (i) a
XX      therapeutic polypeptide sequence (TP) from an intracellular protein that
XX      alters a cellular process when FP enters the cell, and (ii) a
XX      transcellular polypeptide sequence (TCP) that promotes transcytosis of
XX      FP. The FP consists of at least one CDK-binding motif and a TCP. See
XX      AAX26220 for detailed uses of the recombinant transfection system. The
XX      present sequence represents a human truncated p27/p16 fusion protein.
XX
XX      Sequence      252 AA:
XX
XX      Query Match      81.8%; Score 121; DB 20; Length 252;
XX      Best Local Similarity 100.0%; Pred. No. 2.5e-108;
XX      Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      28 ALPNAPNSTYGRPRIOVMWMSARVAELLHGAEPNCADPATLTRPVHDAAREGFDLTV 87
XX      |||||||
XX      Db 132 alpnapnsygrprpqvmwmsarvaeellllhgaepncadpatltrpvhdaaregfldtlv 191
XX
XX      QY 88 VLHRAGARLDVDAWGRIPVDLAEEIGHRDVARYLRAAAGTSGSNHARIDAEGSPSDIP 147
XX      |||||||
XX      Db 192 vlhragarlvdvdaawgrlvpdlaeelghrdvarylraaagtlrsgsnharidaegpsdip 251
XX
XX      QY 148 D 148
XX      |
XX      Db 252 d 252

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```

RESULT 37
AA97535
ID AAY97535 standard; Protein; 252 AA.
XX
AC AAY97535;
XX
DT 15-JAN-2001 (first entry)
XX
DE Human W10 protein sequence.
XX
KW Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;
adenovirus E4 protein; neoplasia; W10 protein.
XX
OS Homo sapiens.
XX
PN WO200052184-A1.
XX
PD 08-SEP-2000.
XX
PR 01-MAR-2000; 2000WO-US05350.
XX
PR 01-MAR-1999; 99US-0122974.
PR 08-APR-1999; 99US-0128271.
PR 09-APR-1999; 99US-0128515.
XX
PA (CELL-) CELL GENESYS INC.
PA (MITO-) MITOTIX INC.
XX
PI Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;
DR MPI: 2000-587315/55.
DR N-PSDB; AAA90932.
XX
XX
PT Protein and nucleic acid compositions for preventing and treating
PT neoplasias (particularly cancer), comprises a novel chimeric cyclin
PT dependent kinase inhibitor and adenovirus E4 protein -
XX
XX
PS Example 1; Page 120; 126pp; English.
XX
XX
CC This sequence represents the human W10 protein.
CC The invention relates to a protein composition comprising a novel
CC purified chimeric cyclin dependent kinase inhibitor (CDK1) and a
CC purified adenovirus E4 protein. The compositions comprising the protein,
CC or the DNA encoding, it are useful for treating neoplasias in animals. The
CC compositions also find use in assays to eliminate a specific
CC sub-population of cultured cells, to determine the susceptibility of
CC neoplastic cells to treatment with the compositions and also in assays to
CC synchronise cell growth in cultured cells.
XX
SQ Sequence 252 AA:

```

```

XX
AC AAY96050;
XX
DT 05-DEC-2000 (first entry)
XX
DE Antiproliferative truncated p27-p16 fusion protein W10.
XX
KW Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; p27; INK4;
KW p16; human; smooth muscle cell; hyperproliferation; restenosis;
KW vasotropic; antiproliferative; gene therapy; mutant; mutein.
XX
OS Homo sapiens.
XX
PN Synthetic.
XX
FH Key
FH Peptide
FT 1..11
FT /label= Haemagglutinin_epitope
FT 12..80
FT /label= p27(12-178)
FT Peptide
FT 81..95
FT /label= Hinge
FT 108..252
FT /label= p16
XX
PN WO200052159-A1.
XX
PD 08-SEP-2000.
XX
PR 28-FEB-2000; 2000WO-US04971.
XX
PR 01-MAR-1999; 99US-0122974.
PR 05-NOV-1999; 99US-0163682.
PR 09-DEC-1999; 99US-0457568.
XX
PA (CELL-) CELL GENESYS INC.
PA (MITO-) MITOTIX INC.
XX
PI McArthur J, Gyuris J, Finer M;
DR MPI: 2000-594183/56.
DR N-PSDB; AAA50497.
XX
PT Novel recombinant lentivirus for inhibiting proliferation of smooth
PT muscle cells in e.g. restenosis, is replication deficient and comprises
PT a transgene encoding a cyclin dependent kinase inhibitor -
XX
XX
PS Example 1; Page 116-117; 126pp; English.
XX
CC The present sequence is that of W10 fusion protein comprising a
CC haemagglutinin tag, a truncated human p27 protein (see AAY96048) in
CC which only the cyclin dependent kinase inhibitor (CDK1) domain is
CC retained, a (Gly4Ser)3 hinge, and human p16 protein (see AAY96053). A
CC claimed method for inhibiting smooth muscle cell hyperproliferation
CC involves transducing smooth muscle cells with a replication-deficient
CC recombinant adenovirus that lacks functional E1 and E4 regions, and
CC comprises a transgene encoding a CDK1. The CDK1 is selected from
CC an INK4 family protein such as human p16, a CIP/KIP family protein
CC such as p27, active fragments of these, or fusion proteins
CC comprising (active fragments of) an INK4 family protein and a
CC CIP/KIP family protein (see AAY96046 and AAY96049). The method is used
CC to inhibit mammalian smooth muscle cell hyperproliferation induced
CC by injury caused by angioplasty, stent placement or vein
CC engraftment. It is useful for treating vascular pathologies e.g.,
CC restenosis. Also claimed are recombinant lentiviruses encoding
CC CDK1s. Use of truncated p27 was designed to increase the protein's
CC half-life and to eliminate potential phosphorylation sites involved
CC in the negative regulation of CDK1 activity. The p27-p16 fusion
CC proteins interact with the CDK4/cyclinD, CDK2/cyclinA and
CC CDK2/cyclin complexes and inhibit cell cycle progression at
CC multiple points.
XX
SQ Sequence 252 AA:

```

Query Match 81.8%; Score 121; DB 21; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAFVALLLHGAEPCADPATLTTRPVHDAAREGFLDTLV 87  
 |||  
 Db 132 alpnapnsygrpiqymmmgsarvae11llhgaepncadpatlttrpvhdaaregfltdtlv 191  
 |||  
 QY 88 VLHRAGARLDVRDANGRLPYVDLAEEIGHRDVARYLRAAAGTGRGSHNARIDAAREGSPDIP 147  
 |||  
 Db 192 vlhragarldvrdawgrlpyvdlaeeighrdvarylraaagtrgshnaridaaegpsdip 251  
 |||  
 QY 148 D 148  
 +  
 Db 252 d 252

RESULT 39  
 AAY96077  
 AAY96077 standard; Protein; 252 AA.

AC AAY96077;  
 DT 05-DEC-2000 (first entry)  
 DE Angiogenesis inhibitor p27(25-93)-p16 fusion W10.  
 XX  
 XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; human; p27;  
 KW angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;  
 KW endometriosis; psoriasis; vascular retinopathy; cytostatic;  
 KW antiarthritic; antirheumatic; gynaecological; antipsoriatic;  
 KW antiproliferative; gene therapy; mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..11  
 FT Protein /label= Haemagglutinin\_epitope  
 FT /label= p27(12-178)  
 FT Peptide 81..95  
 FT /label= Hinge  
 FT 108..252  
 FT Protein /label= p16  
 PN MO200052158-A1.  
 XX  
 XX 08-SEP-2000.  
 PF 28-FEB-2000; 2000WO-US04970.  
 XX  
 XX 01-MAR-1999; 99US-0122974.  
 PR 05-NOV-1999; 99US-0163682.  
 PR 09-DEC-1999; 99US-0457646.  
 XX  
 XX (CELL-) CELL GENESYS INC.  
 PA (MITO-) MITOTIX INC.  
 XX  
 PI Patel S, Mcarthur J, Gyuris J;  
 XX  
 DR MPI: 2000-565501/52.  
 DR N-PSDB; AAA50532.  
 XX  
 PT Inhibiting angiogenesis and treating angiogenesis-associated  
 PT conditions, e.g. neoplasia, psoriasis by transducing an endothelial  
 PT cell with a recombinant virus having a transgene encoding a cyclin  
 PT dependent kinase inhibitor -  
 XX  
 PS Example 1; Page 124-125; 138pp; English.  
 CC The present sequence is that of fusion protein W10 comprising an

CC N-terminal haemagglutinin tag, a truncated human p27 protein (see  
 CC AAY96075) in which only the cyclin dependent kinase inhibitor domain  
 CC is retained, a (Gly4Ser)3 hinge, and human p16 protein (see AAY96067).  
 CC A claimed method for inhibiting angiogenesis involves transducing an  
 CC epithelial cell with a transgene encoding a cyclin dependent kinase  
 CC inhibitor (CDK1). The delivery system is a liposome or a recombinant  
 CC virus. The CDK1 is a protein of the CIP/KIP family such as p27, a  
 CC protein of the INK4 family such as p16, active fragments of these  
 CC (e.g. amino acids 25-93 or 12-178 of human p27), or a fusion protein  
 CC comprising 2 CDK1 proteins such as (truncated) p27 and p16 (see  
 CC AAY96068-80). The method is used to treat conditions associated with  
 CC angiogenesis, e.g. neoplasia, rheumatoid arthritis, endometriosis,  
 CC psoriasis and vascular retinopathy (claimed). Alternatively, the  
 CC transgene is delivered to an auxiliary cell, and is expressed by  
 CC that cell such that the CDK1 is released into the blood and  
 CC contacts the target epithelial cell. Use of truncated p27 was  
 CC designed to increase the protein's half-life and to eliminate  
 CC potential phosphorylation sites involved in the negative  
 CC regulation of CDK1 activity.  
 CC  
 CC Sequence 252 AA;  
 XX  
 XX S0

Query Match 81.8%; Score 121; DB 21; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAFVALLLHGAEPCADPATLTTRPVHDAAREGFLDTLV 87  
 |||  
 Db 132 alpnapnsygrpiqymmmgsarvae11llhgaepncadpatlttrpvhdaaregfltdtlv 191  
 |||  
 QY 88 VLHRAGARLDVRDANGRLPYVDLAEEIGHRDVARYLRAAAGTGRGSHNARIDAAREGSPDIP 147  
 |||  
 Db 192 vlhragarldvrdawgrlpyvdlaeeighrdvarylraaagtrgshnaridaaegpsdip 251  
 |||  
 QY 148 D 148  
 +  
 Db 252 d 252

RESULT 40  
 AAY96079  
 ID AAY96079 standard; Protein; 323 AA.  
 XX  
 AC AAY96079;  
 XX  
 DT 05-DEC-2000 (first entry)  
 DE Secretable angiogenesis inhibitor p27(25-93)-p16 fusion W9.  
 XX  
 XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; human; p27;  
 KW angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;  
 KW endometriosis; psoriasis; vascular retinopathy; cytostatic;  
 KW antiarthritic; antirheumatic; gynaecological; antipsoriatic;  
 KW antiproliferative; gene therapy; HIV; protein secretion; mutant;  
 mutein.  
 XX  
 XX Chimeric - Homo sapiens.  
 OS Chimeric - Human immunodeficiency virus.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 97..166  
 FT Protein /label= p27(25-93)  
 FT /label= p16  
 FT /label= p16  
 PN MO200052158-A1.  
 XX  
 XX 08-SEP-2000.  
 PF 28-FEB-2000; 2000WO-US04970.  
 XX

PR 01-MAR-1999; 99US-0122974.  
 PR 05-NOV-1999; 99US-0163682.  
 PR 09-DEC-1999; 99US-0457646.  
 PA (CELL-) CELL GENESYS INC.  
 PA (MITO-) MITOTIX INC.  
 PI Patel S, Meathur J, Gyuris J;  
 DR WPI; 2000-565501/52.  
 DR N-PSDB; AAA50534.  
 XX  
 PT Inhibiting angiogenesis and treating angiogenesis-associated  
 PT conditions, e.g. neoplasia, psoriasis by transducing an endothelial  
 PT cell with a recombinant virus having a transgene encoding a cyclin  
 PT dependent kinase inhibitor  
 PS  
 PS Disclosure: Page 130-131; 138pp; English.

CC The present sequence is that of a secretable, internalizable form  
 CC of cyclin dependent kinase inhibitor (CDK1) W9. This version of W9  
 CC differs from that of AAY96076 by the inclusion of the proinsulin  
 CC leader sequence and a translocation sequence from HIV tat amino  
 CC acids 1-72. W9 (see AAY96076) comprises a truncated human p27 protein  
 CC (see AAY96075) in which only the cyclin dependent kinase inhibitor  
 CC (CDK1) domain is retained, and the human p16 protein (see AAY96067).  
 CC A claimed method for inhibiting angiogenesis involves transducing  
 CC an epithelial cell with a transgene encoding a CDK1. The CDK1  
 CC delivery system is a liposome or a recombinant virus. The CDK1  
 CC is a protein of the GIP/KIP family such as p27, a protein of the  
 CC INK4 family such as p16, active fragments of these proteins (e.g.  
 CC amino acids 25-93 or 12-178 of human p27), or a fusion protein  
 CC comprising 2 CDK1 proteins such as (truncated) p27 and p16 (see  
 CC AAY96068-80). A method in which the CDK1 is W9 is specifically  
 CC claimed. The method is used to treat conditions associated with  
 CC angiogenesis, e.g. neoplasia, rheumatoid arthritis, endometriosis,  
 CC psoriasis and vascular retinopathy (claimed). Alternatively, the  
 CC transgene is delivered to an auxiliary cell, and is expressed by  
 CC that cell such that the CDK1 is released into the blood and  
 CC contacts the target epithelial cell. Use of truncated p27 was  
 CC designed to increase the protein's half-life and to eliminate  
 CC potential phosphorylation sites involved in the negative  
 CC regulation of CDK1 activity.

Sequence 323 AA:

Query Match 81.8%; Score 121; DB 21; Length 323;  
 Best Local Similarity 100.0%; Pred. No. 3, 1e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNANSGRRPIQVMMGSAVAELLHGAEPNCADPATLTRPVHDAREGFLDTLV 87  
 Db |  
 Db 203 alpnapnsygrripdyymmmgsarvae11llhgaepncadpatltrpvhdaregfltdlv 262  
 QY 88 VLHRAGARLDVDRAMGRPLPVDLAEEIGHRDVARYLRAAAGTRGSHARIDAAEGSPDIP 147  
 Db |  
 Db 263 vlhragarldvdrdawgrlpyvdlaeeighrdvarylraaagtrgsharidaaegpsdip 322  
 QY 148 D 148  
 Db |  
 Db 323 d 323

RESULT 41

AAW95103

AAW95103 standard; Protein; 334 AA.

25-MAY-1999 (first entry)

Truncated p27/p16 fusion protein.

XX  
 KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; retransosis;  
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;  
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;  
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;  
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;  
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;  
 KW tachycardia; human; p27; p16; truncated.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W09906540-A2.  
 XX  
 XX 11-FEB-1999.  
 XX  
 XX 29-JUL-1998; 98WO-US15759.  
 XX  
 XX 29-JUL-1997; 97US-0902572.  
 XX  
 XX (MITO-) MITOTIX INC.  
 XX  
 XX Beach DH, Gyuris J, Lamphere L;  
 XX  
 XX WPI; 1999-153770/13.  
 XX  
 XX N-PSDB; AAX26231.  
 XX  
 PS Claim 63; Page 83; 88pp; English.

CC The invention relates to novel inhibitors of cyclin-dependent kinases  
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant  
 CC transfection system (A) that comprises: (i) first gene construct  
 CC comprising a sequence encoding an inhibitory polypeptide containing at  
 CC least one CDK-binding motif for binding and inhibiting activity of a  
 CC CDK, linked to a transcription regulator functional in eukaryotic cells;  
 CC (ii) second gene construct comprising a sequence encoding a polypeptide  
 CC that promotes endothelialisation, and (iii) a gene delivery composition  
 CC for delivering the GCs to a cell for transfection. Also provided are  
 CC nucleic acids encoding a fusion protein (FP) containing: (i) a  
 CC therapeutic polypeptide sequence (TP) from an intracellular protein that  
 CC alters a cellular process when FP enters the cell, and (ii) a  
 CC transcellular polypeptide sequence (TCP) that promotes transcytosis of  
 CC FP. The FP consists of at least one CDK-binding motif and a TCP. See  
 CC AAX26220 for detailed uses of the recombinant transfection system. The  
 CC present sequence represents a human truncated p27/p16 fusion protein.

Sequence 334 AA:

Query Match 81.8%; Score 121; DB 20; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 3, 2e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNANSGRRPIQVMMGSAVAELLHGAEPNCADPATLTRPVHDAREGFLDTLV 87  
 Db |  
 Db 214 alpnapnsygrripdyymmmgsarvae11llhgaepncadpatltrpvhdaregfltdlv 273  
 QY 88 VLHRAGARLDVDRAMGRPLPVDLAEEIGHRDVARYLRAAAGTRGSHARIDAAEGSPDIP 147  
 Db |  
 Db 274 vlhragarldvdrdawgrlpyvdlaeeighrdvarylraaagtrgsharidaaegpsdip 333  
 QY 148 D 148  
 Db |  
 Db 334 d 334

RESULT 42

AAW97532

AAW97532 standard; Protein; 334 AA.

```

XX AC AAY97532;
XX DT 15-JAN-2001 (first entry)
XX DE Human W8 protein sequence.
XX KW Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;
XX KM adenovirus E4 protein; neoplasia; W8 protein.
XX OS Homo sapiens.
XX PN WO200052184-A1.
XX PD 08-SEP-2000.
XX PF 01-MAR-2000; 2000WO-US05350.
XX PR 01-MAR-1999; 99US-0122974.
XX PR 08-APR-1999; 99US-0128271.
XX PR 09-APR-1999; 99US-0128515.
XX PA (CELL-) CELL GENESYS INC.
XX PA (MITO-) MITOTIX INC.
XX PI Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;
XX PI WPI: 2000-587315/55.
XX DR N-PSDB: AAA90929.
XX PT Protein and nucleic acid compositions for preventing and treating
XX PT neoplasias (particularly cancer), comprises a novel chimeric cyclin
XX PT dependent kinase inhibitor and adenovirus E4 protein -
XX PS Example 1; Page 117-118; 126pp; English.
XX CC This sequence represents the human W8 protein.
XX CC The invention relates to a protein composition comprising a novel
XX CC purified chimeric cyclin dependent kinase inhibitor (CDK1) and a
XX CC purified adenovirus E4 protein. The compositions comprising the protein,
XX CC or the DNA encoding it are useful for treating neoplasias in animals. The
XX CC compositions also find use in assays to eliminate a specific
XX CC sub-population of cultured cells, to determine the susceptibility of
XX CC neoplastic cells to treatment with the compositions and also in assays to
XX CC synchronise cell growth in cultured cells.
XX SQ Sequence 334 AA.
XX
XX Query Match 81.8%; Score 121; DB 21; Length 334;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-108;
XX Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 28 ALPNANSGRRPIQYMMGSAFVALLLHGAEPNCADPATLTTPVHDAEGLDLY 87
XX DB 214 alpnapnsygrlpdyymmmgsarvaeillllhgaepncadpaltltpvhaaregltdlty 273
XX QY 88 VLRRACARLDVRDAMGRPLPYDLAEELGHRDVARYLRAAGTRGSHARIDAEGPSDIP 147
XX DB 274 vlrragarlvdrrdamgrlpydlaeelghrdvarylraaagtrgsharidaaegpsdip 333
XX QY 148 D 148
XX DB 334 d 334
XX
XX RESULT 43
XX ID AAY96047
XX AC AAY96047;
XX DT 05-DEC-2000 (first entry)

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```

XX DE Antiproliferative truncated p27-p16 fusion protein W8.
XX KW Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; p27; INK4;
XX KW p16; human; smooth muscle cell; hyperproliferation; restenosis;
XX KW vasotropic; antiproliferative; gene therapy; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Peptide 1..11
XX FT /Label= Haemagglutinin_epitope
XX FT Protein 12..176
XX FT /Label= p27(12-178)
XX FT Protein 177..334
XX FT /Label= p16
XX PN WO200052159-A1.
XX PD 08-SEP-2000.
XX PF 28-FEB-2000; 2000WO-US04971.
XX PR 01-MAR-1999; 99US-0122974.
XX PR 05-NOV-1999; 99US-0163682.
XX PR 09-DEC-1999; 99US-0457568.
XX PA (CELL-) CELL GENESYS INC.
XX PA (MITO-) MITOTIX INC.
XX PI McArthur J, Gyuris J, Finer M;
XX PI WPI: 2000-594183/56.
XX DR N-PSDB: AAA50494.
XX PT Novel recombinant lentivirus for inhibiting proliferation of smooth
XX PT muscle cells in e.g. restenosis, is replication deficient and comprises
XX PT a transgene encoding a cyclin dependent kinase inhibitor -
XX PS Example 1; Page 113-114; 126pp; English.
XX CC The present sequence is that of W8 fusion protein comprising an
XX CC N-terminal haemagglutinin tag, a truncated human p27 protein (see
XX CC AAY96045) in which the first 12 N-terminal and the final 21 C-terminal
XX CC amino acids of full-length p27 (see AAY96052) are deleted, and a
XX CC C-terminal human p16 protein (see AAY96053), with no (Gly/Ser)3 hinge.
XX CC A claimed method for inhibiting smooth muscle cell hyperproliferation
XX CC involves transducing smooth muscle cells with a replication-deficient
XX CC recombinant adenovirus that lacks functional E1 and E4 regions, and
XX CC comprises a transgene encoding a cyclin dependent kinase inhibitor
XX CC (CDK1). The CDK1 is an INK4 family protein such as human p16, a
XX CC CIP/KIP family protein such as p27, active fragments of these, or
XX CC fusion proteins comprising (active fragments of) an INK4 family
XX CC protein and a CIP/KIP family protein (see AAY96046 and AAY96049). The
XX CC method is used to inhibit mammalian smooth muscle cell
XX CC hyperproliferation induced by injury caused by angioplasty, stent
XX CC placement or vein engraftment. It is useful for treating vascular
XX CC pathologies e.g. restenosis. Also claimed are recombinant
XX CC lentiviruses encoding CDK1s. Use of truncated p27 was designed to
XX CC increase the protein's half-life and to eliminate potential
XX CC phosphorylation sites involved in the negative regulation of CDK1
XX CC activity. The p27-p16 fusion proteins interact with the
XX CC CDK4/cyclinD, CDK2/cyclinA and CDK2/cyclinE complexes and inhibit
XX CC cell cycle progression at multiple points.
XX SQ Sequence 334 AA.
XX
XX Query Match 81.8%; Score 121; DB 21; Length 334;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-108;
XX Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



QY 28 ALPNAPNSYGRPRPIQVMMGSAARVAEILLHGAEPCADPATLTRPVHDAAREGFIDTLV 87  
 CC |||||||  
 CC 214 alpnapnsygrprpqymmggsarvaeilllhgaepncadpatltrpvhaaregfldtlv 273  
 CC |||||||  
 QY 88 VLRHAGARLDVDRDAGRLPYDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAGPSDIP 147  
 CC |||||||  
 CC 274 vlrhagarldvdawgrlpydlaeelghrdvarylrtaaagtrgsnharidaaegpsdip 333  
 CC |||||||  
 QY 148 D 148  
 CC |  
 CC 334 d 334  
 Db  
 RESULT 44  
 AAY96074  
 ID AAY96074 standard; Protein: 334 AA.  
 AC AAY96074;  
 XX  
 XX 05-DEC-2000 (first entry)  
 DE Angiogenesis inhibitor p27(12-178)-p16 fusion W8.  
 XX  
 XX  
 KM Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; human; p27;  
 KM angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;  
 KM endometriosis; psoriasis; vascular retinopathy; cytostatic;  
 KM antiarthritic; antirheumatic; gynaecological; antipsoriatic;  
 KM antiproliferative; gene therapy; mutant; mutain.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..11  
 FT /label= Haemagglutinin epitope  
 FT Protein 12..176  
 FT /label= p27(12-178)  
 FT 177..334  
 FT Protein /label= p16  
 PN WO20052158-A1.  
 PD 08-SEP-2000.  
 XX  
 XX 28-FEB-2000; 2000WO-US04970.  
 PF  
 XX 01-MAR-1999; 99US-0122974.  
 PR 05-NOV-1999; 99US-0163682.  
 PR 09-DEC-1999; 99US-0457646.  
 XX  
 XX (CELL-) CELL GENESYS INC.  
 PA (MITO-) MITOTIX INC.  
 XX  
 XX Patel S, Mcarthur J, Gyuris J;  
 DR WPI: 2000-565501/52.  
 DR N-PSDB: AAA50529.  
 XX  
 PT Inhibiting angiogenesis and treating angiogenesis-associated  
 PT conditions, e.g. neoplasia, psoriasis by transducing an endothelial  
 PT cell with a recombinant virus having a transgene encoding a cyclin  
 PT dependent kinase inhibitor -  
 XX  
 XX Example 1; Page 120-122; 138pp; English.  
 PS  
 XX  
 CC The present sequence is that of fusion protein W8 comprising an  
 CC N-terminal haemagglutinin tag, a truncated human p27 protein (see  
 CC AAY96072) in which the first 12 N-terminal and the final 21  
 CC C-terminal amino acids of full-length p27 (see AAY96066) are deleted,  
 CC and a C-terminal human p16 protein (see AAY96067). A claimed method  
 CC for inhibiting angiogenesis involves transducing an epithelial cell  
 CC with a transgene encoding a cyclin dependent kinase inhibitor (CDK1).  
 CC The delivery system is a liposome or a recombinant virus. The CDK1

CC is a protein of the CIP/KIP family such as p27, a protein of the  
 CC INK4 family such as p16, active fragments of these (e.g. amino acids  
 CC 25-93 or 12-178 of human p27), or a fusion protein comprising 2 CDK1  
 CC proteins such as (truncated) p27 and p16 (see AAY96068-80). The  
 CC method is used to treat conditions associated with angiogenesis,  
 CC e.g. neoplasia, rheumatoid arthritis, endometriosis, psoriasis and  
 CC vascular retinopathy (claimed). Alternatively, the transgene is  
 CC delivered to an auxiliary cell, and is expressed by that cell such  
 CC that the CDK1 is released into the blood and contacts the target  
 CC epithelial cell. Use of truncated p27 was designed to increase the  
 CC protein's half-life and to eliminate potential phosphorylation sites  
 CC involved in the negative regulation of CDK1 activity.  
 XX  
 SQ Sequence 334 AA:  
 QY 28 ALPNAPNSYGRPRPIQVMMGSAARVAEILLHGAEPCADPATLTRPVHDAAREGFIDTLV 87  
 CC |||||||  
 CC 214 alpnapnsygrprpqymmggsarvaeilllhgaepncadpatltrpvhaaregfldtlv 273  
 CC |||||||  
 QY 88 VLRHAGARLDVDRDAGRLPYDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAGPSDIP 147  
 CC |||||||  
 CC 274 vlrhagarldvdawgrlpydlaeelghrdvarylrtaaagtrgsnharidaaegpsdip 333  
 CC |||||||  
 QY 148 D 148  
 CC |  
 CC 334 d 334  
 Db  
 RESULT 45  
 AAM23536  
 ID AAM23536 standard; Protein: 365 AA.  
 AC AAM23536;  
 XX  
 XX 16-MAR-1998 (first entry)  
 DE CDK inhibitory fusion protein p16p27.  
 XX  
 XX  
 KM Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gene;  
 KM chimeric polypeptide; human; binding motif; proliferation control;  
 KM cell differentiation; cell-cycle inhibitor; proliferative disorder;  
 KM tissue degeneration; therapy.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO9727297-A1.  
 PD 31-JUL-1997.  
 XX  
 XX 17-JAN-1997; 97WO-US00569.  
 PF  
 XX 23-JAN-1996; 96US-0589981.  
 PR  
 XX (MITO-) MITOTIX INC.  
 PA  
 PI Beach D, Gyuris J, Lamphere L;  
 DR WPI: 1997-393685/36.  
 DR N-PSDB: AAT74053.  
 XX  
 PT Chimeric inhibitor of cyclin dependent kinase - useful for gene  
 PT therapy of cancer and other proliferative and differentiative  
 PT diseases  
 XX  
 XX Claim 40; Page 46-48; 58pp; English.  
 CC This sequence represents a chimeric polypeptide of the invention. It was  
 CC derived from a fusion of the human p27 and p16 cDNA sequences. The

CC chimeric polypeptides of the invention have cyclin-dependent kinase (CDK)  
 CC binding motifs from at least two different proteins that bind to CDKs.  
 CC The protein controls proliferation and/or differentiation of cells,  
 CC particularly they inhibit cell-cycle progression. They can be used to  
 CC treat a wide range of proliferative disorders, e.g. cancer, leukemia,  
 CC psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They  
 CC can also treat diseases associated with de-differentiation or  
 CC degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's  
 CC diseases, gastric ulcers and autonomous diseases of the peripheral  
 CC nervous system. Other applications include reducing growth of hair and  
 CC protecting hair follicle cells against cytotoxic treatments, cosmetically  
 CC to treat various forms of folliculitis, and to inhibit spermatogenesis or  
 CC oogenesis. The chimeric proteins can also be used in vitro to maintain  
 CC cells, especially neurons intended for testing specific activity of  
 CC trophic factors, at selected points in the cell cycle. The proteins are  
 CC more active inhibitors of the CDK/cyclin complex than binding motifs used  
 CC individually (since they may bind to CDK involved in different stages of  
 CC the cell cycle).

CC Sequence 365 AA;

Query Match 81.8%; Score 121; DB 16; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAFYAEILLHGAEPNCADPATLTPVYDAAREGFLDTLV 87

Db 46 alpnapnsygrripqymmmgsarvaeilllthgaepncadpatltpvhdaregflidtlv 105

QY 88 VLHRAGARLDVBDAMGRLPVDLAELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 147

Db 106 vlhragarldvbdawgrlpvdlaeelghrdvarylraaagtgsgsnharidaegpsdip 165

QY 148 D 148

Db 166 d 166

RESULT 46

AAW95107

AC AAW95107;

DT 25-MAY-1999 (first entry)

DF Human p16p27 fusion protein.

KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;  
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;  
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;  
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;  
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;  
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;  
 KW tachycardia; human; p27; p16.

XX Homo sapiens.

XX MO9906540-A2.

XX 11-FEB-1999.

XX 29-JUL-1998; 98WO-US15759.

XX 29-JUL-1997; 97US-0902572.

XX (MITO-) MITOTIX INC.

XX Beach, DH, Gyuris J, Lamphere L;

XX WPI; 1999-153770/13.

DR N-PsDB; AAW6235.

XX Fusion and chimeric proteins including cyclin-dependent kinase  
 PT binding motif - used for regulation of cell proliferation and  
 PT differentiation, for treatment of, e.g. vascular injury, cancers,  
 PT fibrosis and neurodegeneration

XX Claim 63; Page 86; 88pp; English.

XX The invention relates to novel inhibitors of cyclin-dependent kinases  
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant  
 CC transfection system (A) that comprises: (i) first gene construct  
 CC comprising a sequence encoding an inhibitory polypeptide containing at  
 CC least one CDK-binding motif for binding and inhibiting activity of a  
 CC CDK, linked to a transcription regulator functional in eukaryotic cells;  
 CC (ii) second gene construct comprising a sequence encoding a polypeptide  
 CC that promotes endothelialisation, and (iii) a gene delivery composition  
 CC for delivering the GCS to a cell for transfection. Also provided are  
 CC nucleic acids encoding a fusion protein (FP) containing: (i) a  
 CC therapeutic polypeptide sequence (TP) from an intracellular protein that  
 CC alters a cellular process when FP enters the cell, and (ii) a  
 CC transcellular polypeptide sequence (TCP) that promotes transcytosis of  
 CC FP. The FP consists of at least one CDK-binding motif and a TCP. See  
 CC AAX62220 for detailed uses of the recombinant transfection system. The  
 CC present sequence represents a human p16p27 fusion protein.

XX Sequence 365 AA;

Query Match 81.8%; Score 121; DB 20; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAFYAEILLHGAEPNCADPATLTPVYDAAREGFLDTLV 87

Db 245 alpnapnsygrripqymmmgsarvaeilllthgaepncadpatltpvhdaregflidtlv 304

QY 88 VLHRAGARLDVBDAMGRLPVDLAELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 147

Db 305 vlhragarldvbdawgrlpvdlaeelghrdvarylraaagtgsgsnharidaegpsdip 364

QY 148 D 148

Db 365 d 365

RESULT 47

AAW95096

AC AAW95096;

DT 25-MAY-1999 (first entry)

DE Human p16p27 fusion protein.

XX Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;  
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;  
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;  
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;  
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;  
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;  
 KW tachycardia; human; p27; p16.

XX Homo sapiens.

XX MO9906540-A2.

XX 11-FEB-1999.

XX 29-JUL-1998; 98WO-US15759.

XX 29-JUL-1997; 97US-0902572.

PA (MITO-), MITOTIX INC.  
 XX Beach DH, Gyuris J, Lamphere L;  
 PL WPI; 1999-153770/13.  
 DR N-PSDB; AAX26224.  
 XX  
 PT Fusion and chimeric proteins including cyclin-dependent kinase  
 PT binding motif - used for regulation of cell proliferation and  
 PT differentiation, for treatment of, e.g. vascular injury, cancers,  
 PT fibrosis and neurodegeneration  
 XX  
 PS Claim 63; Page 78-79; 88pp; English.  
 XX  
 CC The invention relates to novel inhibitors of cyclin-dependent kinases  
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant  
 CC transfection system (A) that comprises: (i) first gene construct  
 CC comprising a sequence encoding an inhibitory polypeptide containing at  
 CC least one CDK-binding motif for binding and inhibiting activity of a  
 CC CDK, linked to a transcription regulator functional in eukaryotic cells;  
 CC (ii) second gene construct comprising a sequence encoding a polypeptide  
 CC that promotes endothelialisation, and (iii) a gene delivery composition  
 CC for delivering the GCs to a cell for transfection. Also provided are  
 CC nucleic acids encoding a fusion protein (FP) containing: (i) a  
 CC therapeutic polypeptide sequence (TP) from an intracellular protein that  
 CC alters a cellular process when FP enters the cell, and (ii) a  
 CC transcellular polypeptide sequence (TCP) that promotes transcytosis of  
 CC FP. The FP consists of at least one CDK-binding motif and a TCP. See  
 CC AAX26220 for detailed uses of the recombinant transfection system. The  
 CC present sequence represents a human p16p27 fusion protein.  
 XX  
 SO Sequence 365 AA;  
 50

Query Match 81.8%; Score 121; DB 20; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQYMMGSAFVAELLLHGAEPNCADPATLTRPVHDAREGFLDTLV 87  
 |||||||  
 DB 46 alpnapnsygrripqymmgssarvae11llhgaepncadpatltrpvhdaregfltdtlv 105  
 |||||||  
 QY 88 VLRHAGARLDVPRAMGRPLVDLAELIGHRDVARYLRRAAGGTRGSNHARIDAAGPSDIP 147  
 |||||||  
 DB 106 vlhagarlidvrdawgrlpydlaee1ghrdvarylraaaggrtgsnharidaaegpsdip 165  
 |||||||  
 QY 148 D 148  
 ||  
 DB 166 d 166  
 ||

RESULT 48  
 AAY97527  
 ID AAY97527 standard; Protein: 365 AA.  
 XX  
 AC AAY97527;  
 XX  
 DT 15-JAN-2001 (first entry)  
 XX  
 DE Human W4 protein sequence.  
 XX  
 KW Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;  
 KW adenovirus E4 protein; neoplasia; W4 protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200052184-A1.  
 XX  
 PD 08-SEP-2000.  
 XX  
 PF 01-MAR-2000; 2000WO-US05350.  
 XX  
 PR 01-MAR-1999; 99US-0122974.  
 PR

PR 08-APR-1999; 99US-0128271.  
 PR 09-APR-1999; 99US-0128515.  
 XX  
 PA (CELL-) CELL GENESYS INC.  
 PA (MITO-) MITOTIX INC.  
 XX  
 PI Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;  
 XX  
 DR WPI; 2000-587315/55.  
 DR N-PSDB; AAA90924.  
 XX  
 PT Protein and nucleic acid compositions for preventing and treating  
 PT neoplasias (particularly cancer), comprises a novel chimeric cyclin  
 PT dependent kinase inhibitor and adenovirus E4 protein -  
 XX  
 PS Example 1; Page 110-111; 126pp; English.  
 XX  
 CC This sequence represents the human W4 protein.  
 CC The invention relates to a protein composition comprising a novel  
 CC purified chimeric cyclin dependent kinase inhibitor (CDK1) and a  
 CC purified adenovirus E4 protein. The compositions comprising the protein,  
 CC or the DNA encoding it are useful for treating neoplasias in animals. The  
 CC compositions also find use in assays to eliminate a specific  
 CC sub-population of cultured cells, to determine the susceptibility of  
 CC neoplastic cells to treatment with the compositions and also in assays to  
 CC synchronise cell growth in cultured cells.  
 CC  
 XX  
 SO Sequence 365 AA;  
 50

Query Match 81.8%; Score 121; DB 21; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQYMMGSAFVAELLLHGAEPNCADPATLTRPVHDAREGFLDTLV 87  
 |||||||  
 DB 245 alpnapnsygrripqymmgssarvae11llhgaepncadpatltrpvhdaregfdltlv 304  
 |||||||  
 QY 88 VLRHAGARLDVPRAMGRPLVDLAELIGHRDVARYLRRAAGGTRGSNHARIDAAGPSDIP 147  
 |||||||  
 DB 305 vlhagarlidvrdawgrlpydlaee1ghrdvarylraaaggrtgsnharidaaegpsdip 364  
 |||||||  
 QY 148 D 148  
 ||  
 DB 365 d 365  
 ||

RESULT 49  
 AAY97529  
 ID AAY97529 standard; Protein: 365 AA.  
 XX  
 AC AAY97529;  
 XX  
 DT 15-JAN-2001 (first entry)  
 XX  
 DE Human W6 protein sequence.  
 XX  
 KW Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;  
 KW adenovirus E4 protein; neoplasia; W6 protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200052184-A1.  
 XX  
 PD 08-SEP-2000.  
 XX  
 PF 01-MAR-2000; 2000WO-US05350.  
 XX  
 PR 01-MAR-1999; 99US-0122974.  
 PR 08-APR-1999; 99US-0128271.  
 PR 09-APR-1999; 99US-0128515.  
 XX  
 PA (CELL-) CELL GENESYS INC.

PA (MITO-) MITOTIX INC.  
 XX  
 XX Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;  
 XX WPI; 2000-587315/55.  
 DR N-PSDB: AAA90926.  
 XX  
 XX Protein and nucleic acid compositions for preventing and treating  
 PT neoplasias (particularly cancer), comprises a novel chimeric cyclin  
 PT dependent kinase inhibitor and adenovirus E4 protein -  
 XX  
 XX Example 1: Page 113-114; 126pp: English.  
 PS  
 CC This sequence represents the human W6 protein.  
 CC The invention relates to a protein composition comprising a novel  
 CC purified chimeric cyclin dependent kinase inhibitor (CDK1) and a  
 CC purified adenovirus E4 protein. The compositions comprising the protein,  
 CC or the DNA encoding it are useful for treating neoplasias in animals. The  
 CC compositions also find use in assays to eliminate a specific  
 CC sub-population of cultured cells, to determine the susceptibility of  
 CC neoplastic cells to treatment with the compositions and also in assays to  
 CC synchronise cell growth in cultured cells.  
 XX  
 SQ Sequence 365 AA:  
 XX  
 Query Match 81.8%; Score 121; DB 21; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 28 ALPNAPNSYGRRIQVMMGSAFVAELLHGAEPNCADPATLTRPVHDAREGFLDTLV 87  
 DB 46 alpnapnsygrripqymmgasrvaellllhgaepncadpatltrpvhdaregfltdtlv 105  
 QY 88 VLRAGARLDVDAWGRLPYDLAEELGHRDVARIRLAAAGGTGSGNHARIDAEGPSDIP 147  
 DB 106 vlhragarldvrdawgrlpydlaeelghrdvairlraaaggtgrsnharidaegpsdip 165  
 QY 148 D 148  
 DB 166 d 166  
 RESULT 50  
 AAY96042  
 ID AAY96042 standard; Protein; 365 AA.  
 XX  
 AC AAY96042;  
 XX  
 XX 05-DEC-2000 (first entry)  
 DE Antiproliferative p27-p16 fusion protein W4.  
 XX  
 XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; p27; INK4;  
 KM p16; human; smooth muscle cell; hyperproliferation; restenosis;  
 KM vasotrophic; antiproliferative; gene therapy.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..11  
 FT Protein /label= Haemagglutinin\_tag  
 FT Protein 12..208  
 FT Protein /label= p27  
 FT Protein 212..365  
 FT Protein /label= p16  
 FT Misc-difference 15  
 FT /note= "encoded by CGA"  
 FT Misc-difference 149  
 FT /note= "encoded by GAG"  
 XX  
 PN WO200052199-A1.

XX  
 PD 08-SEP-2000.  
 XX  
 PF 28-FEB-2000; 2000MO-US04971.  
 XX  
 PR 01-MAR-1999; 99US-0122974.  
 PR 05-NOV-1999; 99US-0163682.  
 PR 09-DEC-1999; 99US-0457568.  
 XX  
 PA (CELL-) CELL GENESYS INC.  
 PA (MITO-) MITOTIX INC.  
 XX  
 PI McArthur J, Gyuris J, Finer M;  
 XX  
 DR WPI; 2000-594183/56.  
 DR N-PSDB: AAA50489.  
 XX  
 XX Novel recombinant lentivirus for inhibiting proliferation of smooth  
 PT muscle cells in e.g. restenosis, is replication deficient and comprises  
 PT a transgene encoding a cyclin dependent kinase inhibitor -  
 XX  
 XX Example 1: Page 103-105; 126pp: English.  
 PS  
 XX The present sequence is that of p27-p16 fusion protein W4 comprising  
 CC an N-terminal haemagglutinin tag, the human p27 protein (see AAY96052),  
 CC and the human p16 protein (see AAY96053), with no (Gly4Ser)3 hinge.  
 CC It is encoded by a nucleic acid obtained by PCR amplification of p27  
 CC and p16 DNAs. A claimed method for inhibiting smooth muscle cell  
 CC hyperproliferation involves transducing smooth muscle cells with a  
 CC replication-deficient recombinant adenovirus that lacks functional  
 CC E1 and E4 regions, and comprises a transgene encoding a cyclin  
 CC dependent kinase inhibitor (CDK1). The CDK1 is selected from an  
 CC INK4 family protein such as human p16, a CIP/KIP family protein  
 CC such as p27, active fragments of these, or fusion proteins  
 CC comprising (active fragments of) an INK4 family protein and a  
 CC CIP/KIP family protein (see AAY96046 and AAY96049). The method is used  
 CC to inhibit mammalian smooth muscle cell hyperproliferation, induced  
 CC by injury caused by angioplasty, stent placement or vein  
 CC engraftment. It is useful for treating vascular pathologies e.g.,  
 CC restenosis. Also claimed are recombinant lentiviruses encoding  
 CC CDK1s.  
 XX  
 SQ Sequence 365 AA:  
 XX  
 Query Match 81.8%; Score 121; DB 21; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 28 ALPNAPNSYGRRIQVMMGSAFVAELLHGAEPNCADPATLTRPVHDAREGFLDTLV 87  
 DB 245 alpnapnsygrripqymmgasrvaellllhgaepncadpatltrpvhdaregfltdtlv 304  
 QY 88 VLRAGARLDVDAWGRLPYDLAEELGHRDVARIRLAAAGGTGSGNHARIDAEGPSDIP 147  
 DB 305 vlhragarldvrdawgrlpydlaeelghrdvairlraaaggtgrsnharidaegpsdip 364  
 QY 148 D 148  
 DB 365 d 365  
 Search completed: September 19, 2002, 17:28:32  
 Job time: 245 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:27:07 ; Search time 16.1 Seconds  
(without alignments)  
883.306 Million cell updates/sec

Title: US-09-016-869B-35

Perfect score: 148  
Sequence: 1 MEPSADWLTATAARGVEEV.....TRGSNHRARIDAAEGSPDIPD 148

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

W size: 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :  
1: pIR1:\*  
2: pIR2:\*  
3: pIR3:\*  
4: pIR4:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121	81.8	156	2 JE0141	cyclin dependent k
2	72	48.6	138	2 B53479	CDK4 inhibitor p14
3	48	32.4	130	2 I78845	p15INK4b - mouse
4	34	23.0	41	2 I52720	gene p15INK4B prot
5	19	12.8	167	2 I58352	p16INK4a - mouse
6	8	5.4	334	2 G69303	iron (III) ABC tra
7	8	5.4	390	2 T43647	hypothetical prote
8	8	5.4	1691	1 A44212	genome polypeptide
9	8	5.4	1693	1 MNMWH	genome polypeptide
10	7	4.7	138	2 AD1515	hypothetical prote
11	7	4.7	138	2 A11156	hypothetical prote
12	7	4.7	141	2 AB1892	hypothetical prote
13	7	4.7	142	2 B72683	hypothetical prote
14	7	4.7	154	1 A70792	hypothetical prote
15	7	4.7	160	2 E34768	ORF3 protein - Orf
16	7	4.7	164	2 A57378	Cdk4/CDK6 inhibito
17	7	4.7	166	2 A57379	Cdk4/CDK6 inhibito
18	7	4.7	166	2 B57378	cyclin-dependent k
19	7	4.7	171	2 E97641	hypothetical prote
20	7	4.7	171	2 AF2864	acetyltransferase
21	7	4.7	173	2 A11885	hypothetical prote
22	7	4.7	195	2 T36141	probable nicotinam
23	7	4.7	205	2 C89814	hypothetical prote
24	7	4.7	216	2 AH3203	Rhb family transp
25	7	4.7	223	1 B23724	alcohol dehydrogen
26	7	4.7	223	1 C23724	alcohol dehydrogen
27	7	4.7	223	1 D23724	alcohol dehydrogen
28	7	4.7	227	2 A75304	ABC transporter A
29	7	4.7	229	2 H83425	probable enoyl-CoA

30	7	4.7	230	2 A95886	probable transcrip
31	7	4.7	231	2 D69880	purine nucleoside
32	7	4.7	251	2 F82977	transcription regu
33	7	4.7	254	1 DEFERL	alcohol dehydrogen
34	7	4.7	254	1 A40553	alcohol dehydrogen
35	7	4.7	254	1 S15711	alcohol dehydrogen
36	7	4.7	254	1 S15712	alcohol dehydrogen
37	7	4.7	254	1 S06001	alcohol dehydrogen
38	7	4.7	254	1 B24268	alcohol dehydrogen
39	7	4.7	254	1 A24268	alcohol dehydrogen
40	7	4.7	254	1 S01901	alcohol dehydrogen
41	7	4.7	254	1 E23724	alcohol dehydrogen
42	7	4.7	254	2 A23724	alcohol dehydrogen
43	7	4.7	254	2 D72464	hypothetical prote
44	7	4.7	273	2 T34740	hypothetical prote
45	7	4.7	278	2 F87289	molibdenum transp
46	7	4.7	283	2 E84258	hypothetical prote
47	7	4.7	314	2 D70313	riboflavin kinase
48	7	4.7	318	1 F70536	3',5'-cyclic-nucle
49	7	4.7	331	2 D86413	cysteine proteinas
50	7	4.7	333	2 JC7713	ankyrin-repeat pro
51	7	4.7	334	2 A82751	ABC transporter AT
52	7	4.7	345	2 B84752	probable cysteine
53	7	4.7	346	2 C86413	cysteine proteinas
54	7	4.7	348	2 T18230	alcohol dehydrogen
55	7	4.7	353	2 T35450	ABC transporter AT
56	7	4.7	353	2 D75553	branched-chain am
57	7	4.7	363	2 E75457	probable phosphata
58	7	4.7	364	2 C70777	probable cobC - My
59	7	4.7	365	2 F86413	probable cysteine
60	7	4.7	389	2 E82618	hypothetical prote
61	7	4.7	405	2 F86314	protein F2H15.16 l
62	7	4.7	413	2 D70668	probable transposa
63	7	4.7	462	2 B75306	probable cyclopro
64	7	4.7	464	2 AE2650	glutamine syntheta
65	7	4.7	466	1 MNMWH	capsid protein ICP
66	7	4.7	479	2 D97432	probable glutamine
67	7	4.7	504	2 B98159	argininosuccinate
68	7	4.7	504	2 AG3128	argininosuccinate
69	7	4.7	507	2 C97499	guanosine-5'-triph
70	7	4.7	507	2 AH2717	exopolysphatase
71	7	4.7	512	2 AF3402	hypothetical prote
72	7	4.7	520	2 C70311	hypothetical prote
73	7	4.7	523	2 C70717	probable purif prot
74	7	4.7	527	1 ORSEUB	stib protein - Ser
75	7	4.7	527	2 T37055	probable oxidoredu

#### ALIGNMENTS

RESULT 1  
JE0141  
N:Alternate names: CDK4 inhibitor p16 (INK4A/MTS1); cyclin-dependent kinase inhibitor  
C:Species: Homo sapiens (man)  
C:Date: 02-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 19-May-2000  
C:Accession: JE0141; I59268; S39359; I59585; JC5679  
R:Huang, C.G.; Deng, W.; Fu, J.L.  
Chin, J. Biotechnol. 13: 105-107, 1997  
A:Title: Molecular cloning and sequencing of p16 ink4 cDNA from hela cell.  
A:Reference number: JE0141  
A:Accession: JE0141  
A:Molecule type: mRNA  
A:Residues: 1-156 <HUA>  
A:Experimental source: Hella cell  
R:Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagiwara, K.; Hussain, S.P.; Bennett,  
Proc. Natl. Acad. Sci. U.S.A. 91, 11045-11049, 1994  
A:Title: Mutations and altered expression of p16INK4 in human cancer.  
A:Reference number: I59268; WUID:95062202  
A:Accession: I59268  
A:Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA

A:Residues: 1-152 <KAM>  
 A:Cross-references: GB:L27211; NID:9558656; PIDN:AAA92554.1; PID:9558657  
 A:Note: the sequence is revised in Genbank entry HUMINK4X, release 113.0, PIDN:AAA92554.1  
 R:Serano, M.; Hannon, G.J.; Beach, D.  
 Nature 366, 704-707, 1993  
 A:Title: A new regulatory motif in cell-cycle control causing specific inhibition of cyclin D  
 A:Reference number: S39359; MUID:94081956  
 A:Accession: S39359  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 9-34, 'V', 36-156 <SER>  
 A:Note: this sequence is corrected in reference I59268  
 R:Ram, A.; Gruts, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.; Science 264, 436-440, 1994  
 A:Title: A cell cycle regulator potentially involved in genesis of many tumor types.  
 A:Reference number: I59585; MUID:94204645  
 A:Accession: I59585  
 A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 51-152 <KAM>  
 A:Cross-references: GB:S69804; NID:9546272; PIDN:AAD14048.1; PID:94261748  
 A:Note: This protein inhibits the activity of cyclin D1/CDK4 and cyclin D1/CDK6 kinase  
 C:Genetics:  
 A:Gene: GDB:CDKN2A; CDK4I; MCM; P16; INK4; MTS1; CMM2; CDKN2  
 A:Cross-references: GDB:335362; OMIM:600160  
 A:Map position: 9p21-9p21  
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology  
 C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

Query Match 81.8%; Score 121; DB 2; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-111;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPRIOYMMGSAVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87  
 DB 36 ALPNAPNSYGRPRIOYMMGSAVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLV 95

QY 88 VLHRAGARLDVDRDAGRLPVDLAELGHRDVARVLRPAAGGTGSGNHARIDAEGSPDIP 147  
 DB 96 VLHRAGARLDVDRDAGRLPVDLAELGHRDVARVLRPAAGGTGSGNHARIDAEGSPDIP 155

QY 148 D 148  
 DB 156 D 156

RESULT 2  
 79 Inhibitor p14(INK4B/MTS2) - human  
 N:Alternate names: CDK6-associated protein p15(INK4B); cyclin-dependent kinase inhibitor  
 C:Species: Homo sapiens (man)  
 C:Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 21-Jul-2000  
 C:Accession: B55479; S47593; I81183; I52713  
 R:Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.; Genes Dev. 8, 2939-2952, 1994  
 A:Title: Growth suppression by p18, a p16(INK4/MTS1) - and p14(INK4B/MTS2)-related CDK6 A  
 A:Reference number: A55479; MUID:95095079  
 A:Accession: B55479  
 A:Molecule type: mRNA  
 A:Residues: 1-138 <GUA>  
 A:Cross-references: GB:U17075; NID:9639715; PIDN:AAC50075.1; PID:9639716  
 A:Experimental source: HeLa cells  
 R:Hannon, G.J.; Beach, D.  
 Nature 371, 257-261, 1994  
 A:Title: p15(INK4B) is a potential effector of TGF-beta-induced cell cycle arrest.  
 A:Reference number: S47593; MUID:94359613  
 A:Accession: S47593  
 A:Molecule type: mRNA  
 A:Residues: 1-19, 'TP', 22-24-31, 'HSW', 35-138 <HAN>  
 A:Cross-references: GB:I36844; NID:9556197; PIDN:AAA50282.1; PID:9556198  
 A:Experimental source: HeLa cells  
 R:Kamb, A.; Gruts, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.; St

Science 264, 436-440, 1994  
 A:Title: A cell cycle regulator potentially involved in genesis of many tumor types.  
 A:Reference number: I59585; MUID:94204645  
 A:Accession: I81183  
 A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 53-138 <KAM>  
 A:Cross-references: GB:S69805; NID:9546273; PIDN:AAD14049.1; PID:94261749  
 R:Jen, J.; Harper, J.W.; Bigner, S.H.; Bigner, D.D.; Papadopoulos, N.; Markowitz, S.; Cancer Res. 54, 6353-6358, 1994  
 A:Title: Deletion of p16 and p15 genes in brain tumors.  
 A:Reference number: I52713; MUID:95079408  
 A:Accession: I52713  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-52 <RES>  
 A:Cross-references: GB:S75756; NID:9861470; PIDN:AAD14186.1; PID:94261886  
 C:Genetics:  
 A:Gene: GDB:CDKN2B; MTS2  
 A:Cross-references: GDB:579577; OMIM:600431  
 A:Map position: 9p21-9p21  
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology  
 C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

Query Match 48.6%; Score 72; DB 2; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-63;  
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IOVMMGSAVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLVLRAGARLDVDR 100  
 DB 51 IOVMMGSAVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLVLRAGARLDVDR 110

QY 101 AMGRLPVDAE 112  
 DB 111 AMGRLPVDAE 122

RESULT 3  
 178845 p15INK4B - mouse  
 C:Species: Mus sp. (mouse)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 19-May-2000  
 C:Accession: I78845  
 R:Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H. Oncogene 11, 635-645, 1995  
 A:Title: Cloning and characterization of murine p16INK4a and p15INK4b genes.  
 A:Reference number: I58352; MUID:95380169  
 A:Accession: I78845  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-130 <RES>  
 A:Cross-references: GB:S79252; NID:91087092; PID:91087093  
 C:Genetics:  
 A:Gene: p15INK4B  
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

Query Match 32.4%; Score 48; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-39;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 VAEILLHGAEPNCADPATLTRPVHDAAREGFLDTLVLRAGARLDV 98  
 DB 53 VAEILLHGAEPNCADPATLTRPVHDAAREGFLDTLVLRAGARLDV 100

RESULT 4  
 152720 gene p15INK4B protein - rat (fragment)  
 C:Species: Rattus sp. (rat)  
 C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 26-May-2000  
 C:Accession: I52720

R:Knapek, D.F.; Serrano, M.; Beach, D.; Trono, D.; Walker, C.L.  
 Cancer Res. 55, 1607-1612, 1995  
 A>Title: Association of rat p15INK4B/p16INK4 deletions with monosomy 5 in kidney epithel  
 A:Reference number: 152720; MUID:95228036  
 A:Accession: 152720  
 A>Status: preliminary; translated from GB/EMBL/DDJ  
 A:Molecule type: DNA  
 A:Residues: 1-41 <RES>  
 A:Cross-references: GB:S77734; NID:g998711  
 C:Genetics:  
 A:Gene: p15INK4B  
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

Query Match 23.0%; Score 34; DB 2; Length 41;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-26;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 VAEILLHGAPNCADPATLTRPVHDAAREGFLD 84  
 |||  
 8 VAEILLHGAPNCADPATLTRPVHDAAREGFLD 41

RESULT 5  
 I58352  
 p16INK4a - mouse  
 C:Species: Mus sp. (mouse)  
 C>Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 24-Nov-1999  
 C:Accession: I58352  
 R:Quelle, D.E.; Ashmun, R.A.; Hannou, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.; W  
 Oncogene 11, 635-645, 1995  
 A>Title: Cloning and characterization of murine p16INK4a and p15INK4b genes.  
 A:Reference number: I58352; MUID:95380169  
 A:Accession: I58352  
 A>Status: preliminary; translated from GB/EMBL/DDJ  
 A:Molecule type: mRNA  
 A:Residues: 1-167 <RES>  
 A:Cross-references: GB:S79251; NID:g1087090; PID:g1087091  
 C:Genetics:  
 A:Gene: p16INK4a  
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

Query Match 12.8%; Score 19; DB 2; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-11;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 RPVHDAAREGFLDLYVLH 90  
 |||  
 1 71 RPVHDAAREGFLDLYVLH 89

RESULT 6  
 G69303  
 Iron (III) ABC transporter, permease protein (hemu-1) homolog - Archaeoglobus fulgidus  
 C:Species: Archaeoglobus fulgidus  
 C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Aug-1999  
 C:Accession: G69303  
 R:Rienk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
 Nature 390, 364-370, 1997  
 A:Authors: Uetebach, T.; Cotton, M.D.; Spijgs, T.; Atriach, P.; Kaine, B.P.; Sykes, S.  
 Smith, H.O.; Moese, C.R.; Venter, J.C.  
 A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
 A:Reference number: A69250; MUID:98049343  
 A:Accession: G69303  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-334 <RES>  
 A:Cross-references: GB:AE001075; GB:AE000782; NID:g2689398; PIDN:AA890806.1; PID:g265020  
 C:Superfamily: vitamin B12 transport protein btuc

Query Match 5.4%; Score 8; DB 2; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 7.1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 RVAELLIL 57  
 |||  
 Db 9 RVAELLIL 16

RESULT 7  
 T43647  
 hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)  
 C:Species: Schizosaccharomyces pombe  
 C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000  
 C:Accession: T43647  
 R:Lee, M.; Yoo, H.S.; Chung, K.S.  
 Submitted to the EMBL Data Library, February 1998  
 A:Description: Clone 17 (blind homologue).  
 A:Reference number: 222596  
 A:Accession: T43647  
 A>Status: preliminary; translated from GB/EMBL/DDJ  
 A:Molecule type: mRNA  
 A:Residues: 1-390 <LEE>  
 A:Cross-references: EMBL:AF049529; PIDN:AAD02493.1

Query Match 5.4%; Score 8; DB 2; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 8.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 122 LRAAAGT 129  
 |||  
 Db 15 LRAAAGT 22

RESULT 8  
 A44212  
 genome polypeptide - hepatitis E virus (strain Mexico)  
 N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)  
 C:Species: hepatitis E virus  
 C>Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 19-Jan-2001  
 C:Accession: A44212; B48547  
 R:Huang, C.C.; Nguyen, D.; Fernandez, J.; Yun, K.Y.; Fry, K.E.; Bradley, D.W.; Tam, A  
 Virology 191, 550-558, 1992  
 A>Title: Molecular cloning and sequencing of the Mexico isolate of hepatitis E virus  
 A:Reference number: A44212; MUID:93079857  
 A:Accession: A44212  
 A:Molecule type: genomic RNA  
 A:Residues: 1-1691 <HUA>  
 A:Cross-references: GB:M74506; NID:g330017; PIDN:AAA45730.1; PID:g330018  
 R:Fry, K.E.; Tam, A.W.; Smith, M.M.; Kim, J.P.; Luk, K.C.; Young, L.M.; Platack, M.; F  
 Virus Genes 6, 173-185, 1992  
 A>Title: Hepatitis E virus (HEV): strain variation in the nonstructural gene region e  
 A:Reference number: A48547; MUID:92271462  
 A:Accession: B48547  
 A:Molecule type: genomic RNA  
 A:Residues: 965-1691 <Fry>  
 A>Note: sequence extracted from NCBI backbone (NCBIN:104576, NCBI:104578)  
 C:Superfamily: hepatitis E virus nonstructural protein  
 C:Keywords: ATP; GTP binding; nonstructural protein; nucleotide binding; nucleotidylt  
 F:973-980/Region: nucleotide-binding motif A (P-loop)  
 F:979/Binding site: ATP/GTP (Lys) #status predicted

Query Match 5.4%; Score 8; DB 1; Length 1691;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 109 LAELIGHR 116  
 |||  
 Db 1243 LAELIGHR 1250

## RESULT 9

genome polyprotein - hepatitis E virus (strain Burma)  
N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)  
C:Species: hepatitis E virus  
C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 23-Jul-1999  
C:Accession: A40778; A48547  
R:Ram, A.W.; Smith, M.M.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.  
Virology 185, 120-131, 1991  
A:Title: Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length viral genome  
A:Reference number: A40778; MUID:92024067  
A:Accession: A40778  
A:Molecule type: genomic RNA  
A:Residues: 1-1693 <TAM>  
A:Cross-references: GB:M73218; NID:9330023; PIDN:AAA45734.1; PID:9330024  
R:Fry, K.E.; Tam, A.W.; Smith, M.M.; Kim, J.P.; Luk, K.C.; Young, L.M.; Piatk, M.; Feld  
Virus Genes 6, 173-185, 1992  
A:Title: Hepatitis E virus (HEV): strain variation in the nonstructural gene region encoded  
Reference number: A48547; MUID:92271462  
C:Accession: A48547  
A:Molecule type: genomic RNA  
A:Residues: 967-1693 <FRY>  
A:Cross-references: GB:M32400; NID:9330021; PIDN:AAA03206.1; PID:9330022  
A:Note: sequence extracted from NCBI backbone (NCBIN:104572, NCBI:104573)  
C:Superfamily: hepatitis E virus nonstructural protein  
C:Keywords: ATP; nonstructural protein; nucleotidyltransferase

Query Match 5.4%; Score 8; DB 1; Length 1693;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 109 LAEELGHR 116  
|||||  
DB 1245 LAEELGHR 1252

## RESULT 10

hypothetical protein lin0660 [imported] - *Listeria innocua* (strain Clijp11262)  
C:Species: *Listeria innocua*  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AD1515  
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, H.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Ma  
C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.  
A:Title: Comparative genomics of *Listeria* species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AD1515  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-138 <GIA>  
A:Cross-references: GB:AL592022; PIDN:CAC95892.1; PID:g16413100; GSPDB:GN00178  
C:Genetics:  
A:Gene: lin0660

Query Match 4.7%; Score 7; DB 2; Length 138;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 108 DLAEELG 114  
|||||  
DB 52 DLAEELG 58

RESU: 1  
A115

hypothetical protein lmo0657 [imported] - *Listeria monocytogenes* (strain EGD-e)  
C:Species: *Listeria monocytogenes*  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001

C:Accession: A11156  
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, H.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.  
A:Title: Comparative genomics of *Listeria* species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: A11156  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-138 <GIA>  
A:Cross-references: GB:NC\_003210; PIDN:CAC98735.1; PID:g16410046; GSPDB:GN00177  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: lmo0657

Query Match 4.7%; Score 7; DB 2; Length 138;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 108 DLAEELG 114  
|||||  
DB 52 DLAEELG 58

## RESULT 12

hypothetical protein alr0683 [imported] - *Anabaena* sp. (strain PCC 7120)  
C:Species: *Anabaena* sp.  
A:Note: *Anabaena* sp. (strain PCC 7120) is a synonym of *Nostoc* sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 11-Jan-2002  
C:Accession: AB1892  
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Irigu  
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-Fixing Cyanobacterium  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AB1892  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-141 <KRP>  
A:Cross-references: GB:BA000019; PIDN:BAE72641.1; PID:g17130029; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr0683

Query Match 4.7%; Score 7; DB 2; Length 141;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 109 LAEELGH 115  
|||||  
DB 105 LAEELGH 111

## RESULT 13

hypothetical protein APE0883 - *Aeropyrum pernix* (strain K1)  
C:Species: *Aeropyrum pernix*  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jun-2000  
C:Accession: B72683  
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Tawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.  
DNA Res. 6, 83-101, 1999  
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aero*  
A:Reference number: A72450; MUID:99310339



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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:28:57 ; Search time 11.94 Seconds

(without alignments)  
479,941 Million cell updates/sec

Title: US-09-016-869b-35

Perfect score: 148

Sequence: 1 MEPSADWLATAAARGVEEV.....TRGSNHRIDAECPSDIDP 148

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

W size: 0  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	81.8	156	1	CDN2_HUMAN
2	72	48.6	138	1	CDN5_HUMAN
3	48	32.4	130	1	CDN5_MOUSE
4	36	24.3	130	1	CDN5_RAT
5	19	12.8	167	1	CDN2_MOUSE
6	14	9.5	171	1	CDN2_MONDO
7	8	5.4	747	1	V222_FOWPY
8	8	5.4	1691	1	POLN_HEVME
9	8	5.4	1693	1	POLN_HEVME
10	8	5.4	1693	1	POLN_HEVME
11	8	5.4	1693	1	POLN_HEVME
12	8	5.4	1693	1	POLN_HEVME
13	7	4.7	166	1	CDN7_MOUSE
14	7	4.7	166	1	CDN7_MOUSE
15	7	4.7	231	1	GPH_RHOSH
16	7	4.7	231	1	MTN_BACSV
17	7	4.7	253	1	ADH1_DROH
18	7	4.7	253	1	ADH1_DROH
19	7	4.7	253	1	ADH1_DROH
20	7	4.7	253	1	ADH1_DROH
21	7	4.7	253	1	ADH2_DROH
22	7	4.7	253	1	ADH2_DROH
23	7	4.7	253	1	ADH2_DROH
24	7	4.7	253	1	ADH2_DROH
25	7	4.7	253	1	ADH2_DROH
26	7	4.7	253	1	ADH2_DROH
27	7	4.7	253	1	ADH2_DROH
28	7	4.7	253	1	ADH2_DROH
29	7	4.7	253	1	ADH2_DROH
30	7	4.7	253	1	ADH2_DROH
31	7	4.7	253	1	ADH2_DROH
32	7	4.7	253	1	ADH2_DROH
33	7	4.7	253	1	ADH2_DROH

34	7	4.7	253	1	ADH_DROH	Q00672 drosophila
35	7	4.7	253	1	ADH_DROH	P23361 drosophila
36	7	4.7	253	1	ADH_DROH	P23377 drosophila
37	7	4.7	253	1	ADH_DROH	P23378 drosophila
38	7	4.7	254	1	ADH_DROH	P10807 drosophila
39	7	4.7	295	1	MYRA_MTCR	P37000 micromosp
40	7	4.7	348	1	ADH2_CANAL	Q94038 candida alb
41	7	4.7	364	1	YH31_MYCTU	Q10503 mycobacteri
42	7	4.7	466	1	VP19_HSV2G	P22486 herpes simp
43	7	4.7	466	1	VP19_HSV2H	P89461 herpes simp
44	7	4.7	523	1	PUR8_MYCTU	P71553 m bifunctio
45	7	4.7	527	1	SEF8_SERMA	P21409 serratia ma
46	7	4.7	535	1	Y897_MYCTU	Q10555 mycobacteri
47	7	4.7	575	1	PT1_ECOTI	P08839 escherichia
48	7	4.7	575	1	PT1_ECOTI	P12654 salmonella
49	7	4.7	612	1	YC81_MYCTU	Q11040 mycobacteri
50	7	4.7	676	1	CMC2_MOUSE	Q99xx4 mus musculu
51	7	4.7	700	1	UVRD_MYCTU	Q53344 mycobacteri
52	7	4.7	706	1	UL17_HSVB	P28950 equine herp
53	7	4.7	889	1	C122_HUMAN	Q9b2q6 homo sapien
54	7	4.7	1880	1	ANK1_HUMAN	P16157 homo sapien
55	7	4.7	2194	1	GLSN_MEPSA	Q03460 medicago sa
56	7	4.7	2397	1	MOKB_SCHPO	Q09854 schizosacch
57	6	4.1	102	1	CH15_DROGR	P13425 drosophila
58	6	4.1	116	1	E411_ADEP2	P36708 human adeno
59	6	4.1	120	1	R18E_AERPE	Q9y551 aeropyrum p
60	6	4.1	122	1	FOLB_ECOTI	P31055 escherichia
61	6	4.1	123	1	ATPE_STRLI	P50011 streptomyce
62	6	4.1	124	1	SGP2_CHRVI	Q52179 chromatium
63	6	4.1	126	1	TYRT_STPAL	P55046 streptomyce
64	6	4.1	128	1	CAL1_HUMAN	P06881 homo sapien
65	6	4.1	129	1	RS9_BACSV	P21470 bacillus su
66	6	4.1	130	1	RS9_STAM	Q99552 staphylococ
67	6	4.1	130	1	TRJ5_ECOTI	P17907 escherichia
68	6	4.1	137	1	YCE3_HUMAN	Q9y3e2 homo sapien
69	6	4.1	140	1	R1NA_BPFA	Q03182 bacteriophag
70	6	4.1	141	1	CALO_HUMAN	P01258 homo sapien
71	6	4.1	141	1	HBA_CICCI	P01983 ciconia cic
72	6	4.1	142	1	UP12_ECOTI	P39177 escherichia
73	6	4.1	145	1	Y074_BACAN	Q9rmw0 bacillus an
74	6	4.1	146	1	HBH_CHEKU	P80271 chelodonic
75	6	4.1	147	1	NIRG_PSEST	Q05254 pseudomonas

#### ALIGNMENTS

RESULT 1  
ID CDN2\_HUMAN STANDARD: PRT: 156 AA.  
AC P42771; Q15191;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Cyclin-dependent kinase 4 inhibitor A (CDK4I) (P16-INK4) (P16-INK4A)  
DE (Multiple tumor suppressor 1) (MTS1).  
GN CDKN2A OR CDKN2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94081956; Pubmed=8259215;  
RA Serrano M., Hannon G.J., Beach D.;  
RT "A new regulatory motif in cell-cycle control causing specific  
inhibition of cyclin D/CDK4.";  
RL Nature 366:704-707(1993).  
RN [2]  
RP SEQUENCE OF 51-152 FROM N.A.  
RX MEDLINE=94204645; Pubmed=8153634;  
RA Kamb A., Grus N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,  
Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,

RA Skolnick M.H.;  
 RT "A cell cycle regulator potentially involved in genesis of many tumor  
 RL types."; Science 264:436-440(1994).  
 RN [3]  
 RP SEQUENCE OF 1-20 FROM N.A.  
 RX MEDLINE-9618208; PubMed-8622687;  
 RA Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;  
 RT "Regulation of p16CDKN2 expression and its implications for cell  
 RL immortalization and senescence."; Mol. Cell. Biol. 16:859-867(1996).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.  
 RX MEDLINE-98421670; PubMed-9751050;  
 RA Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;  
 RT "Structural basis for inhibition of the cyclin-dependent kinase Cdk6  
 RL by the tumour suppressor p16INK4a."; Nature 395:237-243(1998).  
 RN [5]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE-20027100; PubMed-10559205;  
 RA Yuan C., Li J., Selby T.L., Byeon I.J., Tsai M.D.;  
 RT "Tumor suppressor INK4: comparisons of conformational properties  
 RL between p16(INK4a) and p18(INK4C)."; J. Mol. Biol. 294:201-211(1999).  
 RN [6]  
 RP REVIEW ON MELANOMA VARIANTS.  
 RX MEDLINE-96377761; PubMed-8783570;  
 RA Dracopoli N.C., Fountain J.W.;  
 RT "CDKN2 mutations in melanoma."; Cancer Surv. 26:115-132(1996).  
 RN [7]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE-96303699; PubMed-8723678;  
 RA Smth-Soerensen B., Hoyvig E.;  
 RT "CDKN2A (p16INK4A) somatic and germline mutations."; Hum. Mutat. 7:294-303(1996).  
 RN [8]  
 RP VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).  
 RX MEDLINE-94338359; PubMed-8060323;  
 RA Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;  
 RT "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41  
 RL (cyclin-dependent kinase-4 inhibitor) gene in human primary non-small  
 RN cell lung carcinomas."; Biochem. Biophys. Res. Commun. 202:1426-1430(1994).  
 RN [9]  
 RP VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 AND  
 RL THR-148. MEDLINE-95078916; PubMed-7987387;  
 RA Hussussian C.J., Struwing J.P., Goldstein A.M., Higgins P.A.T.,  
 RT Ally D.S., Sheahan M.D., Clark W.H., Jr., Tucker M.A., Dracopoli N.C.;  
 RL "Germline p16 mutations in familial melanoma."; Nat. Genet. 8:15-21(1994).  
 RN [10]  
 RP VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.  
 RX MEDLINE-95060835; PubMed-7970734;  
 RA Zhou X., Tarmn L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,  
 RT Abraham J.M., Meltzer S.J.;  
 RL "The MTS1 gene is frequently mutated in primary human esophageal  
 RN tumors."; Oncogene 9:3737-3741(1994).  
 RN [11]  
 RP VARIANTS.  
 RX MEDLINE-95188190; PubMed-7882351;  
 RA Okamoto A., Hussain S.P., Hagiwara K., Spillare F.A., Rusin M.R.,  
 RT Demetrick D.J., Serrano M., Hannon G.J., Shisaki M., Zaitwala M.,  
 RL Bennett W.P., Forester K., Gerwin B., Beach D.H., Harris C.C.;  
 RN "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in  
 RT primary and metastatic lung cancer."; Cancer Res. 55:1448-1451(1995).  
 RN [12]  
 RP VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.  
 RX MEDLINE-96121580; PubMed-8593405;  
 RA Walker G.J., Hussussian C.J., Flores J.F., Glendenning J.M.,  
 RL Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;  
 RT "Mutations of the CDKN2/p16INK4 gene in Australian melanoma  
 RN kindreds."; Hum. Mol. Genet. 4:1845-1852(1995).  
 RN [13]  
 RP CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 AND  
 RL T-148. MEDLINE-95375774; PubMed-7647780;  
 RX Garade K., Hussussian C.J., Sikorski R.S., Varmus H.E.,  
 RA Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,  
 RL Dracopoli N.C.;  
 RN "Mutations associated with familial melanoma impair p16INK4  
 RT function."; Nat. Genet. 10:114-116(1995).  
 RN [14]  
 RP VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68; T-85 AND T-148.  
 RX MEDLINE-96323259; PubMed-8710906;  
 RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., MacDonald D.J.,  
 RA Lucchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,  
 RL Isselbacher K.J., Sober A.J., Haber D.A.;  
 RN "Prevalence of germ-line mutations in p16, p19ARF, and CDK4 in  
 RT familial melanoma: analysis of a clinic-based population."; Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).  
 RN [15]  
 RP VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.  
 RX MEDLINE-97472457; PubMed-9328469;  
 RA Harland M., Meloni R., Guis N., Pinney E., Brookes S., Spurr N.K.,  
 RA Frischau A.-M., Battaille V., Peters G., Cuzick J., Selby P.,  
 RT Bishop D.T., Bishop J.N.;  
 RL "Germline mutations of the CDKN2 gene in UK melanoma families."; Hum. Mol. Genet. 6:2061-2067(1997).  
 RN [16]  
 RP VARIANTS FAMILIAL MELANOMA.  
 RX MEDLINE-98087572; PubMed-9425228;  
 RA Soufir N., Avril M.-F., Chompret A., Demeunais F., Bombléd J.,  
 RA Spatz A., Stoppa-Lyonnet D., Bernard J., Bressac-De Pallierets B.;  
 RT Hum. Mol. Genet. 7:941-941(1998).  
 RN [18]  
 RP VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.  
 RA Gretsdoctir S., Olfedoctir G.H., Borg A.;  
 RT "Five novel somatic CDKN2/p16 mutations identified in melanoma,  
 RL glioma and carcinoma of the pancreas."; Hum. Mutat. 12:212-212(1998).  
 RN [19]  
 RP VARIANTS MELANOMA GLY-59; TYR-84; TRP-87 AND TRP-101.  
 RX MEDLINE-20332815; PubMed-10874641;  
 RA Ruiz A., Puig S., Malveyh J., Lazaro C., Lynch M., Gimenez-Artau A.M.,  
 RT Puig L., Sanchez-Conejo J., Estivill X., Castel T.;  
 RL "CDKN2A mutations in Spanish cutaneous malignant melanoma families and  
 RN patients with multiple melanomas and other neoplasia."; J. Med. Genet. 36:490-493(1999).  
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS  
 CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE  
 CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.  
 CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.  
 CC -1- DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A  
 CC WIDE RANGE OF TISSUES.  
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
 CC INHIBITORS.  
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.  
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RESULT 3
CDN5_MOUSE STANDARD: PRT; 130 AA.
ID AC P55271;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin-dependent kinase 4 inhibitor B (P14-INK4B) (P15-INK4B).
GN CDKN2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95380169; PubMed=7651726;
RA Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
RT "Cloning and characterization of murine p16INK4a and p15INK4b genes.";
RT Oncogene 11:635-643(1995).
[2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J X DBA;
RX MEDLINE=97322242; PubMed=9178896;
RA Malumbres M., de Castro I., Santos J., Melendez B., Manques R.,
RA Serrano M., Pellicer A., Fernandez-Piqueras J.;
RT "Inactivation of the cyclin-dependent kinase inhibitor p15INK4b by
RT deletion and de novo methylation with independence of p16INK4a
RT alterations in murine primary T-cell lymphomas.";
RT Oncogene 14:1361-1370(1997).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
CC -1- INDUCTION: BY TGF-BETA.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
CC -----
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CC -----
CC EMBL: U66085; AAB39833.1; -.
CC EMBL: U66084; AAB39833.1; JOINED.
DR HSSP: P42771; IBI7.
DR MGD: MGI:104737; Cdkn2b.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank. 3.
DR SMART: SM00248; ANK. 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat.
FT REPEAT 5 34 ANK 1.
FT REPEAT 38 66 ANK 2.
FT REPEAT 71 100 ANK 3.
FT REPEAT 104 130 ANK 4.
SO SEQUENCE 130 AA; 13788 MW; 7AAD60FE552BCFE9 CRC64;

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Query Match 32.4%; Score 48; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 51 VAEILLHGAEPCADPATLTRPVDAAREGFLDTLVLRHAGARLDV 98
DB 53 VAEILLHGAEPCADPATLTRPVDAAREGFLDTLVLRHAGARLDV 100

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RESULT 4
CDN5_RAT STANDARD: PRT; 130 AA.
ID AC P55272;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin-dependent kinase 4 inhibitor B (P14-INK4B) (P15-INK4B).
GN CDKN2B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96001392; PubMed=7546221;
RA Hino O., Kobayashi E., Hirayama Y., Kobayashi T., Kubo Y.,
RA Tsuchiya H., Kikuchi Y., Mitani H.;
RT "Molecular genetic basis of renal carcinogenesis in the Eker rat
RT model of tuberosus sclerosis (Tsc2).";
RT Mol. Carcinog. 14:23-27(1995).
[2]
SEQUENCE OF 46-86 FROM N.A.
RX MEDLINE=95228036; PubMed=7712460;
RA Knapek D.F., Serrano M., Beach D., Trono D., Walker C.L.;
RT "Association of rat p15INK4b/p16INK4 deletions with monosomy 5 in
RT kidney epithelial cell lines but not primary renal tumors.";
RT Cancer Res. 55:1607-1612(1995).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
CC INITIATION CODONS IN THE SAME READING FRAME.
CC -1- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN
CC TESTIS, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL
CC KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: S79760; AAB35360.1; -.
CC EMBL: S77734; -. NOT_ANNOTATED_CDS.
DR HSSP: O60773; IAP7.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank. 3.
DR SMART: SM00248; ANK. 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
FT CHAIN 1 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
FT LONG ISOFORM.
FT CHAIN 46 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
FT SHORT ISOFORM.
FT INIT MET 46 46 ANK 1.
FT REPEAT 5 34 ANK 1.
FT REPEAT 38 66 ANK 2.
FT REPEAT 71 100 ANK 3.
FT REPEAT 104 130 ANK 4.
SO SEQUENCE 130 AA; 13748 MW; AC45B21FA69FAD92 CRC64;

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Query Match 24.3%; Score 36; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 7.8e-28;

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Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 VAEILLHGAEPNCADPATLTRPVHARREGFLDTL 86  
Db 53 VAEILLHGAEPNCADPATLTRPVHARREGFLDTL 88

RESULT 5  
CDN2\_MOUSE STANDARD; PRT; 167 AA.  
AC P51480;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
GN Cyclin-dependent kinase 4 inhibitor A (CDK4I) (P16-INK4) (P16-INK4A).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RA MEDLINE=95380169; Pubmed=7651726;  
RA Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D., Richter K.H., Walker C., Beach D., Sherr C.J., Seriano M.;  
RT "Cloning and characterization of murine p16INK4a and p15INK4b genes.";  
RL Oncogene 11:635-645(1995).  
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE REGULATOR OF THE PROLIFERATION OF NORMAL CELLS. INHIBITS THE PHOSPHORYLATION OF THE RETINOBLASTOMA PROTEIN BY CDK4 OR CDK6.  
CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6. PREDOMINANT P16 COMPLEXES  
CC -1- CONTAINED CDK6.  
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.  
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE INHIBITORS.  
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.  
CC -----  
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CC -----  
DR EMBL; L76150; AAA85453.1; -;  
DR HSSP; Q60773; 1AP7.  
DR MGDP; MGI:104738; cdkn2a.  
DR InterPro: IPR002110; ANK.  
DR Pfam: PF00023; ank; 3.  
DR SMART; SM00248; ANK; 1.  
DR PROSITE; PS50088; ANK\_REPEAT; FALSE\_NEG.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.  
FT CHAIN 1 167 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,  
FT LONG ISOFORM.  
FT CHAIN 43 167 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,  
FT CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,  
FT INIT\_MET 43 43 SHORT ISOFORM.  
FT REPEAT 35 63 FOR SHORT ISOFORM.  
FT REPEAT 101 130 ANK 1.  
FT REPEAT 167 17870 ANK 2.  
SQ SEQUENCE 167 AA; 17870 MW; 88C4588A105ECB8F CRC64;

Query Match 12.8%; Score 19; DB 1; Length 167;  
Best Local Similarity 100.0%; Pred. No. 3.3e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 RPVHDARREGFLDTLVYLH 90  
Db 71 RPVHDARREGFLDTLVYLH 89

RESULT 6  
CDN2\_MONDO STANDARD; PRT; 171 AA.  
AC 077617;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
GN Cyclin-dependent kinase 4 inhibitor A (CDK4I) (P16-INK4) (P16-INK4A).  
OS Monodelphis domestica (Short-tailed grey opossum).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.  
OX NCBI\_TaxID=13616;  
RA MEDLINE=95380169; Pubmed=7651726;  
RA Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D., Richter K.H., Walker C., Beach D., Sherr C.J., Seriano M.;  
RT "Cloning and characterization of murine p16INK4a and p15INK4b genes.";  
RL Oncogene 11:635-645(1995).  
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE REGULATOR OF THE PROLIFERATION OF NORMAL CELLS. INHIBITS THE PHOSPHORYLATION OF THE RETINOBLASTOMA PROTEIN BY CDK4 OR CDK6.  
CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY).  
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.  
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE INHIBITORS.  
CC -1- SIMILARITY: CONTAINS 3 ANK REPEATS.  
CC -----  
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CC -----  
DR EMBL; AF064808; AAC23669.1; -;  
DR EMBL; AF064808; AAC23670.1; -;  
DR HSSP; P42771; 1B17.  
DR InterPro: IPR002110; ANK.  
DR Pfam; PF00023; ank; 3.  
DR PROSITE; PS50088; ANK\_REPEAT; 1.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.  
FT CHAIN 1 171 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,  
FT LONG ISOFORM.  
FT CHAIN 35 171 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,  
FT CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,  
FT INIT\_MET 35 35 SHORT ISOFORM.  
FT REPEAT 45 74 FOR SHORT ISOFORM.  
FT REPEAT 78 106 ANK 1.  
FT REPEAT 111 140 ANK 2.  
FT REPEAT 171 18707 ANK 3.  
SQ SEQUENCE 171 AA; 18707 MW; 694264F5D0F4F6CC CRC64;

Query Match 9.5%; Score 14; DB 1; Length 171;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 PVHDARREGFLDTL 86  
Db 115 PVHDARREGFLDTL 128

RESULT 7  
V222\_F0MPV STANDARD; PRT; 747 AA.  
AC Q9J513;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)

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DE Putative ankyrin-repeat protein FPV222.
GN FPV222.
OS Foxpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OX Avipoxvirus.
RN NCBI_TaxID=10261;
RP [1]
RX MEDLINE=20193820; PubMed=10729156;
RA Alfonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus."
RL J. Virol. 74:3815-3831(2000).
CC -1- SIMILARITY: CONTAINS 14 ANK REPEATS.
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CC -----
DR EMBL: AF198100; AAF44566.1; -.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 12.
DR SMART: SM00248; ANK; 9.
DR PROSITE: PS50088; ANK_REPEAT; 7.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR Hypothetical protein; Repeat; ANK repeat.
KW REPEAT
FT REPEAT 38 67 ANK 1.
FT REPEAT 103 132 ANK 2.
FT REPEAT 136 165 ANK 3.
FT REPEAT 169 198 ANK 4.
FT REPEAT 202 231 ANK 5.
FT REPEAT 234 263 ANK 6.
FT REPEAT 294 323 ANK 7.
FT REPEAT 328 357 ANK 8.
FT REPEAT 361 393 ANK 9.
FT REPEAT 397 426 ANK 10.
FT REPEAT 430 460 ANK 11.
FT REPEAT 464 493 ANK 12.
FT REPEAT 495 524 ANK 13.
FT REPEAT 529 559 ANK 14.
SQ SEQUENCE 747 AA; 85303 MW; 55P90AF2855C3D28 CRC64;

Query Match 5.4%; Score 8; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 53 ELLILHGA 60
| | | | | | | |
DB 154 ELLILHGA 161

RESULT 8
POLN_HEVME STANDARD; PRT; 1691 AA.
AC 003495;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Non-structural polypeptide [Contains: RNA-directed RNA polymerase
DE (EC 2.7.7.48); Helicase].
OS Hepatitis E virus (strain Mexico) (HEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage.
OX NCBI_TaxID=31768;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93079857; PubMed=1448913;
RA Huang C.C., Nguyen D., Fernandez J., Yun K.Y., Fry K.E.,
RA Bradley D.W., Tam A.W., Reyes G.R.;
RT "Molecular cloning and sequencing of the Mexico isolate of hepatitis
```

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RT E virus (HEV)."
RL Virology 191:550-558(1992).
RN [2]
RP SEQUENCE OF 965-1691 FROM N.A.
RX MEDLINE=92271462; PubMed=1569964;
RA Fry K.E., Tam A.W., Smith M.M., Kim J.P., Luk K.C., Young L.M.,
RA Platack M., Feldman R.A., Yun K.Y., Pundy M.A., McCaustland K.A.,
RA Bradley D.W., Reyes G.R.;
RT "Hepatitis E virus (HEV): strain variation in the nonstructural gene
RT region encoding consensus motifs for an RNA-dependent RNA polymerase
RT and an ATP/GTP binding site."
RL Virus Genes 6:173-185(1992).
CC -1- MISCELLANEOUS: HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENT OF
CC ENTERICALLY TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
CC -----
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CC -----
DR EMBL: M74506; AAA45730.1; -.
DR PIR: A44212; A44212.
DR MEROPS: C41.001; -.
DR InterPro: IPR002589; Alpp.
DR InterPro: IPR002588; RNA_dep_RNAPol2.
DR InterPro: IPR002588; V_methyltransf.
DR InterPro: IPR000606; Viral_helicase1.
DR Pfam: PF01661; Alpp; 1.
DR Pfam: PF00978; RNA_dep_RNAPol2; 1.
DR Pfam: PF01443; Viral_helicase1; 1.
DR Pfam: PF01660; Vmethyltransf; 1.
DR SMART: SM00506; Alpp; 1.
KW Polypeptide; Transferase; RNA-directed RNA polymerase; Helicase;
KW ATP-binding.
FT NP_BIND 973 980 ATP (POTENTIAL).
SQ SEQUENCE 1691 AA; 185224 MW; DB3F0B2C913F871B CRC64;

Query Match 5.4%; Score 8; DB 1; Length 1691;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 109 LAEELGHR 116
| | | | | | | |
DB 1243 LAEELGHR 1250

RESULT 9
POLN_HEVBU STANDARD; PRT; 1693 AA.
AC P29324;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Non-structural polypeptide [Contains: RNA-directed RNA polymerase
DE (EC 2.7.7.48); Helicase].
OS Hepatitis E virus (strain Burma) (HEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage.
OX NCBI_TaxID=31767;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92024067; PubMed=1926770;
RA Tan A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
RA Fry K.E., Reyes G.R.;
RT "Hepatitis E virus (HEV): molecular cloning and sequencing of the
RT full-length viral genome."
RL Virology 185:120-131(1991).
CC -1- MISCELLANEOUS: HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENT OF
CC ENTERICALLY TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
CC -----
```

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:28:37 ; Search time 26.76 Seconds

(without alignments)  
956.773 Million cell updates/sec

Title: US-09-016-869B-35

Perfect score: 148

Sequence: 1 MESPADWLATRAARGVEEV.....TRGSNARIDAEGPSDIPD 148

Scoring table: OLIGO

Searched: 562222 seqs, 172994929 residues

W size: 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database:

1: SP archaea: \*  
2: SP bacteria: \*  
3: SP fungi: \*  
4: SP human: \*  
5: SP invertebrate: \*  
6: SP mammal: \*  
7: SP mhc: \*  
8: SP organelle: \*  
9: SP phage: \*  
10: SP plant: \*  
11: SP rodent: \*  
12: SP virus: \*  
13: SP vertebrate: \*  
14: SP unclassified: \*  
15: SP virus: \*  
16: SP bacteriophage: \*  
17: SP archaea: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	71.6	106	4 Q9NP05	Q9NP05 homo sapien
2	54	36.5	81	6 Q9GMF2	Q9GMF2 canis faml
3	51	34.5	86	6 Q9XS52	Q9XS52 felis silve
4	48	32.4	102	6 Q9XS51	Q9XS51 felis silve
5	48	32.4	86	11 Q9QUP0	Q9QUP0 mus musculu
6	48	32.4	86	11 Q54846	Q54846 mus musculu
7	48	32.4	86	11 Q9TSL1	Q9TSL1 mus scrofa
8	47	31.8	103	6 Q9TSL1	Q9TSL1 mus scrofa
9	32	21.6	130	11 Q91YP9	Q91YP9 mesocricetu
10	26	17.6	36	4 Q9UPB7	Q9UPB7 mus sapien
11	26	17.6	86	6 Q9TSL0	Q9TSL0 mus sapien
12	26	17.6	116	4 Q9S440	Q9S440 mus sapien
13	19	12.8	112	11 Q9QWH4	Q9QWH4 mus musculu
14	19	12.8	113	11 Q9Z1C2	Q9Z1C2 mus spretus
15	19	12.8	159	11 Q9R023	Q9R023 ratus norv
16	19	12.8	168	11 Q89088	Q89088 mus musculu

17	19	12.8	168	11	P97510	P97510 mus musculu
18	18	12.2	113	11	Q9QWH8	Q9QWH8 mus musculu
19	18	12.2	113	11	Q9QWH7	Q9QWH7 mus musculu
20	18	12.2	113	11	Q9QWH6	Q9QWH6 mus musculu
21	15	10.1	58	6	Q97886	Q97886 mus musculu
22	15	10.1	113	11	Q9QWH5	Q9QWH5 mus musculu
23	14	9.5	21	4	Q9UD00	Q9UD00 mus sapien
24	12	8.1	144	11	Q99PH0	Q99PH0 mesocricetu
25	12	8.1	157	11	Q9EQ33	Q9EQ33 mesocricetu
26	8	5.4	44	11	Q9QJ03	Q9QJ03 mus musculu
27	8	5.4	44	11	Q9Z1C0	Q9Z1C0 mus spretus
28	8	5.4	91	12	Q9WLJ9	Q9WLJ9 hepatitis e
29	8	5.4	124	13	Q9W618	Q9W618 xiphophorus
30	8	5.4	124	13	P70067	P70067 xiphophorus
31	8	5.4	300	12	P89468	P89468 herpes slimp
32	8	5.4	303	16	Q92NR2	Q92NR2 rhizobium m
33	8	5.4	334	17	Q29818	Q29818 archaeoglob
34	8	5.4	390	3	Q94237	Q94237 schizosacch
35	8	5.4	487	12	Q81869	Q81869 hepatitis e
36	8	5.4	544	2	Q9AG77	Q9AG77 streptomyc
37	8	5.4	727	12	Q81873	Q81873 hepatitis e
38	8	5.4	1050	4	Q9H014	Q9H014 homo sapien
39	8	5.4	1060	4	Q96NM4	Q96NM4 homo sapien
40	8	5.4	1205	3	Q9HFR5	Q9HFR5 schizosacch
41	8	5.4	1685	12	Q9E8G6	Q9E8G6 hepatitis e
42	8	5.4	1693	12	Q89444	Q89444 hepatitis e
43	8	5.4	1693	12	Q81862	Q81862 hepatitis e
44	8	5.4	1693	12	Q81344	Q81344 hepatitis e
45	8	5.4	1693	12	Q69410	Q69410 hepatitis e
46	8	5.4	1693	12	Q39221	Q39221 hepatitis e
47	8	5.4	1693	12	Q9WLJ5	Q9WLJ5 hepatitis e
48	8	5.4	1693	12	Q9WC28	Q9WC28 hepatitis e
49	8	5.4	1693	12	Q81876	Q81876 hepatitis e
50	8	5.4	1698	12	Q9YLK3	Q9YLK3 hepatitis e
51	8	5.4	1703	12	Q91116	Q91116 hepatitis e
52	8	5.4	1707	12	Q91VZ9	Q91VZ9 hepatitis e
53	8	5.4	1708	12	Q9YLR1	Q9YLR1 hepatitis e
54	8	5.4	1708	12	Q9YLR10	Q9YLR10 swine hepat
55	8	4.7	41	11	Q9QWT5	Q9QWT5 mus musculu
56	7	4.7	42	11	Q9Z1E8	Q9Z1E8 mus spretus
57	7	4.7	42	11	Q9Z1C3	Q9Z1C3 mus spretus
58	7	4.7	49	11	Q922P7	Q922P7 mus musculu
59	7	4.7	82	5	Q9UBK4	Q9UBK4 liodrosophi
60	7	4.7	124	13	Q9DE56	Q9DE56 fuigu rubrip
61	7	4.7	126	2	Q9L236	Q9L236 streptomyc
62	7	4.7	126	5	Q9W1X0	Q9W1X0 drosophila
63	7	4.7	130	16	Q9BBB4	Q9BBB4 rhizobium l
64	7	4.7	138	16	Q92E01	Q92E01 listeria in
65	7	4.7	139	16	Q92C60	Q92C60 rhizobium m
66	7	4.7	142	17	Q9YDNI	Q9YDNI aeropyrum p
67	7	4.7	149	5	Q95V08	Q95V08 drosophila
68	7	4.7	149	5	Q95V07	Q95V07 drosophila
69	7	4.7	149	5	Q95V05	Q95V05 drosophila
70	7	4.7	149	5	Q95V04	Q95V04 drosophila
71	7	4.7	149	5	Q95V03	Q95V03 drosophila
72	7	4.7	149	5	Q95V02	Q95V02 drosophila
73	7	4.7	149	5	Q95V01	Q95V01 drosophila
74	7	4.7	149	5	Q95V00	Q95V00 drosophila
75	7	4.7	149	5	Q95U29	Q95U29 drosophila

## ALIGNMENTS

RESULT 1  
ID Q9NP05  
AC Q9NP05;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
DE CDK4I PROTEIN (FRAGMENT).  
GN CDK4I.

PRELIMINARY; PRT; 106 AA.

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94203288; PubMed=8152487;
RT Nobori T., Miura K., Wu D.J., Lois A., Takabayashi K., Carson D.A.;
RT "Deletions of the cyclin-dependent kinase-4 inhibitor gene in multiple
human cancers."
RL Nature 368:753-756(1994).
DR EMBL; S69824; AAD14050.1; -.
DR EMBL; S69822; AAD14050.1; JOINED.
DR HSSP; P42771; 1B17.
DR InterPro: IPR002110; ANK.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Repeat.
FT NON_TER
SQ SEQUENCE 106 AA; 11314 MW; 2D59442F956B6A61 CRC64;

Query Match
Best Local Similarity 71.6%; Score 106; DB 4; Length 106;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 VMMGSAARVAELLHLGAEFNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVDRAM 102
DB 1 VMMGSAARVAELLHLGAEFNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVDRAM 60

QY 103 GRLPVDAELGHRDVARVYRAAGSTRGSNARIDAAEGPSDIPD 148
DB 61 GRLPVDAELGHRDVARVYRAAGSTRGSNARIDAAEGPSDIPD 106

RESULT 2
Q9GFM2 PRELIMINARY; PRT; 81 AA.
ID Q9GFM2
AC Q9GFM2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4/6 INHIBITOR-A (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBL_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Venkatrej V.S., Mayor J., Modiano J.F.;
RT "Role of p16/Ink4-a in familial canine cancers."
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF234176; AAG01087.1; -.
DR HSSP; P42771; 1B17.
DR InterPro: IPR002110; ANK.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Kinase; Repeat.
FT NON_TER
FT NON_TER
SQ SEQUENCE 81 AA; 8868 MW; 0E39D8D805BEAC0F CRC64;

Query Match
Best Local Similarity 36.5%; Score 54; DB 6; Length 81;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 TLTTPVHDAREGFLDTLVVLRAGARLDVDRAMGRLPVDAELGHRDVARYL 122
DB 27 TLTTPVHDAREGFLDTLVVLRAGARLDVDRAMGRLPVDAELGHRDVARYL 80

RESULT 3
Q9XS52 PRELIMINARY; PRT; 86 AA.
ID Q9XS52
```

```
AC Q9XS52;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P15/MTS2/CDKN2B (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBL_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-PERIPHERAL BLOOD;
RC Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,
RA Nishigaki K., Matari T., Tsujimoto H., Hasegawa A.;
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
and p15(MTS2/CDKN2B)."
RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010808; BAA33541.1; -.
DR HSSP; P42771; 1B17.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 2.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Repeat.
FT NON_TER
SQ SEQUENCE 86 AA; 9340 MW; A59FF0193290E867 CRC64;

Query Match
Best Local Similarity 34.5%; Score 51; DB 6; Length 86;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 PNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVDRAMGRLPVDAEL 112
DB 20 PNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVDRAMGRLPVDAEL 70

RESULT 4
Q9XS51 PRELIMINARY; PRT; 102 AA.
ID Q9XS51
AC Q9XS51;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P16/CDKN2A/MTS1 (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBL_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-PERIPHERAL BLOOD;
RC Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,
RA Nishigaki K., Matari T., Tsujimoto H., Hasegawa A.;
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
and p15(MTS2/CDKN2B)."
RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010807; BAA33540.1; -.
DR HSSP; P42771; 1B17.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 3.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Repeat.
FT NON_TER
FT NON_TER
SQ SEQUENCE 102 AA; 10824 MW; 26399FF21359F35D CRC64;

Query Match
Best Local Similarity 34.5%; Score 51; DB 6; Length 102;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 PNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVDRAMGRLPVDAEL 112
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Db 20 PNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVBDANGRLPVDLAEE 70

RESULT 5  
Q90P0 PRELIMINARY; PRT; 86 AA.

AC 090P0; 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
GN p15.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-VARIOUS STRAINS;  
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
R Pellicer A., Fernandez-Piqueras J.;  
RL Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
in mouse inbred strains.";  
RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U79639; AAD00234.1; -;  
DR EMBL: U79636; AAD00232.1; -;  
DR HSSP: P42771; 1B17.  
DR InterPro: IPR002110; ANK.  
DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
KW ANK repeat; Cyclin; Kinase; Repeat.  
FT NON\_TER 1 86  
FT SEQUENCE 86 AA; 9269 MW; 509D9B3613251B18 CRC64;

Query Match 32.4%; Score 48; DB 11; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.1e-37;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 VAEILLHGAEPNCADPATLTRPVHDAREGFLDTLVVLRAGARLDV 98  
Db 9 VAEILLHGAEPNCADPATLTRPVHDAREGFLDTLVVLRAGARLDV 56

RESULT 6  
Q54846 PRELIMINARY; PRT; 86 AA.

AC 054846; 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15INK4B (FRAGMENT).  
GN CDKN2B.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-C57BL/6J;  
MDLINE=99124385; PubMed=9927195;  
RA Malumbres M., de Castro I.P., Santos J., Piqueras J.F., Pellicer A.;  
RT "Hypermethylation of the cell cycle inhibitor p15INK4b 3'-untranslated  
region interferes with its transcriptional regulation in primary  
lymphomas.";  
RL Oncogene 18:385-396(1999).  
DR EMBL: AF015460; AAB94534.1; -;  
DR HSSP: P42771; 1B17.  
DR InterPro: IPR002110; ANK.  
DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
KW ANK repeat; Kinase; Repeat.  
FT NON\_TER 1 86

SQ SEQUENCE 86 AA; 9237 MW; 0499DB26144FB6DF CRC64;

Query Match 32.4%; Score 48; DB 11; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.1e-37;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 VAEILLHGAEPNCADPATLTRPVHDAREGFLDTLVVLRAGARLDV 98  
Db 9 VAEILLHGAEPNCADPATLTRPVHDAREGFLDTLVVLRAGARLDV 56

RESULT 7  
Q9Z1C1 PRELIMINARY; PRT; 86 AA.

AC 09Z1C1; 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
GN p15(INK4B).  
OS Mus spretus (Western wild mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10096;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SPRET/EL;  
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
R Pellicer A., Fernandez-Piqueras J.;  
RL Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
in mouse inbred strains.";  
RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U79637; AAD00237.1; -;  
DR HSSP: P42771; 1B17.  
DR InterPro: IPR002110; ANK.  
DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
KW ANK repeat; Kinase; Repeat.  
FT NON\_TER 1 86  
FT SEQUENCE 86 AA; 9269 MW; 509D9B3613251B18 CRC64;

Query Match 32.4%; Score 48; DB 11; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.1e-37;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 VAEILLHGAEPNCADPATLTRPVHDAREGFLDTLVVLRAGARLDV 98  
Db 9 VAEILLHGAEPNCADPATLTRPVHDAREGFLDTLVVLRAGARLDV 56

RESULT 8  
Q9T5Y1 PRELIMINARY; PRT; 103 AA.

AC 09T5Y1; 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR, p16 (FRAGMENT).  
GN CDKN2A.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LARGE WHITE;  
RA Le Chalony C., Hayes H., Frelat G., Geoffroy C.;  
RT "Identification and mapping of swine CDKN2A and CDKN2B exon2  
sequences.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ242787; CAB65454.1; -;

DR HSP: P42771; 1B17.  
DR InterPro: IPR002110; ANK.  
DR Pfam: PF00023; ank; 2.  
DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
KW ANK repeat; Kinase; Repeat.  
FT NON\_TER 1  
FT NON\_TER 103  
SQ SEQUENCE 103 AA; 11023 MW; 5D3ABCC1088DE0B CRC64;

Query Match 31.8%; Score 47; DB 6; Length 103;  
Best Local Similarity 100.0%; Pred. No. 1.le-36;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 DPATLTRPVHDAREGFLDTLVLRAGARLDVARDMGRPLVDLAE 112  
Db 24 DPATLTRPVHDAREGFLDTLVLRAGARLDVARDMGRPLVDLAE 70

RESULT 9  
ID Q91YF9 PRELIMINARY; PRT; 130 AA.  
AC Q91YF9;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE P15INK4B CYCLIN-DEPENDENT KINASE INHIBITOR.  
GN P15INK4B.  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
OX NCBI\_TaxID=10036;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PANCREAS;  
RA Muscarella P., Ulrich A.B., Casto B.C., Moniaux N., Knobloch T.J.,  
RA Witte U.A., Melvin S., Pour P.M., Song H., Gold B., Batra S.K.,  
RA Weghorst C.M.;  
RT "Homologous deletion of p15INK4b/p16INKA Gene Locus in Syrian Golden  
RT Hamster Tumor Cell Lines";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ302037; CAC67498.1; -.  
KW Kinase; Cyclin.  
SQ SEQUENCE 130 AA; 13842 MW; 4C04D3F8C6FP013 CRC64;

Query Match 21.6%; Score 32; DB 11; Length 130;  
Best Local Similarity 100.0%; Pred. No. 2.le-22;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 TLTRPVHDAREGFLDTLVLRAGARLDVARD 100  
Db 71 TLTRPVHDAREGFLDTLVLRAGARLDVARD 102

RESULT 10  
ID Q9UPB7 PRELIMINARY; PRT; 36 AA.  
AC Q9UPB7;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR 2A (FRAGMENT).  
GN CDKN2A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Murthy S.K., Demetrick D.J.;  
RT "Genomic sequence of CDKN2A (p16INK4A) 5' to ORF.";

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF044170; AAD02319.1; -.  
KW Kinase.  
FT NON\_TER 36  
FT NON\_TER 36  
SQ SEQUENCE 36 AA; 3672 MW; BC8919D2B4194ECA CRC64;

Query Match 17.6%; Score 26; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.le-17;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATTAARGVEEVALLAA 26  
Db 9 MEPSADWLATTAARGVEEVALLAA 34

RESULT 11  
ID Q91SY0 PRELIMINARY; PRT; 86 AA.  
AC Q91SY0;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).  
GN CDKN2B.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LARGE WHITE;  
RA Le Chalony C., Hayes H., Frelat G., Geffrotin C.;  
RA Le Chalony C., Hayes H., Frelat G.;  
RT "Identification and mapping of swine cyclin-dependent kinase inhibitor  
RT CDKN2A and CDKN2B exon2 sequences";  
RL Cyogenet. Cell Genet. 88:240-243(2000).  
DR EMBL; AJ242788; CAB65455.1; -.  
DR HSP: P42771; 1B17.  
DR InterPro: IPR002110; ANK.  
DR Pfam: PF00023; ank; 2.  
DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
KW ANK repeat; Kinase; Repeat.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 86 AA; 9286 MW; 16EF7A223293CCF9 CRC64;

Query Match 17.6%; Score 26; DB 6; Length 86;  
Best Local Similarity 100.0%; Pred. No. 6.8e-17;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 PNCADPATLTRPVHDAREGFLDTLV 87  
Db 20 PNCADPATLTRPVHDAREGFLDTLV 45

RESULT 12  
ID Q95440 PRELIMINARY; PRT; 116 AA.  
AC Q95440;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR P12.  
GN P16INK4A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PANCREAS;  
RX MEDLINE=99373016; PubMed=10445844;

RA Robertson K.D., Jones P.A.;  
 RT "Tissue-specific alternative splicing in the human INK4a/ARF cell  
 cycle regulatory locus."  
 RL Oncogene 18:3810-3820(1999).  
 DR EMBL: AF115544; AAD11437.1; -  
 DR InterPro: IPR002110; ANK.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.  
 SQ SEQUENCE 116 AA; 12212 MW; F44DBC8E0EB3A7C8 CRC64;

Query Match 17.6%; Score 26; DB 4; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAARGVEYRALLEA 26  
 |||  
 DB 9 MEPSADWLATAARGVEYRALLEA 34

RESULT 13  
 ID Q9QWH4 PRELIMINARY; PRT; 112 AA.  
 AC Q9QWH4;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
 GN p16(INK4a).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MUS POSCHIAVINUS;  
 RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
 RA Pellicer A., Fernandez-Piqueras J.;  
 RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
 in mouse inbred strains."  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U79635; AAD00231.1; -  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.  
 FT NON\_TER 1  
 FT 112 112  
 SQ SEQUENCE 112 AA; 11956 MW; 65C46A849DCB65F CRC64;

Query Match 12.8%; Score 19; DB 11; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 RPYVDAAREGFLDTLVVH 90  
 |||  
 DB 30 RPYVDAAREGFLDTLVVH 48

RESULT 14  
 ID Q9ZIC2 PRELIMINARY; PRT; 113 AA.  
 AC Q9ZIC2;  
 DT 01-MAY-1999 (Tremblrel. 10, Created)  
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
 GN p16(INK4a).  
 OS Mus spretus (Western wild mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10096;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRET/El;  
 RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
 RA Pellicer A., Fernandez-Piqueras J.;  
 RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
 in mouse inbred strains."  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U79634; AAD00236.1; -  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 2.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.  
 FT NON\_TER 1  
 FT 113 113  
 SQ SEQUENCE 113 AA; 12073 MW; C3BFE8325DB2D79E CRC64;

Query Match 12.8%; Score 19; DB 11; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 RPYVDAAREGFLDTLVVH 90  
 |||  
 DB 30 RPYVDAAREGFLDTLVVH 48

RESULT 15  
 ID Q9R0Z3 PRELIMINARY; PRT; 159 AA.  
 AC Q9R0Z3;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE P16 PROTEIN P16INK4a.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=F344/N; TRISUE=LUNG;  
 RX MEDLINE=97184461; PubMed=9032263;  
 RA Swaford D.S., Middleton S.K., Palmisano W.A., Nikula K.J.,  
 RA Testaigzi J., Baylin S.B., Herman J.G., Belinsky S.A.;  
 RT "Frequent aberrant methylation of p16INK4a in primary rat lung  
 tumors."  
 RL MOL. Cell. Biol. 17:1366-1374(1997).  
 DR EMBL: L81167; AAD48924.1; -  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 4.  
 DR SMART: SM00248; ANK; 1.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Repeat.  
 SQ SEQUENCE 159 AA; 17366 MW; 3C4CA920A1FEAE86 CRC64;

Query Match 12.8%; Score 19; DB 11; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 RPYVDAAREGFLDTLVVH 90  
 |||  
 DB 72 RPYVDAAREGFLDTLVVH 90

RESULT 16  
 ID O89088 PRELIMINARY; PRT; 168 AA.  
 AC O89088;  
 DT 01-NOV-1998 (Tremblrel. 08, Created)

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DT 01-NOV-1998 (TREMblrel. 08, last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE CYCLIN DEPENDENT KINASE INHIBITOR p16INK4a (p16INK4a TUMOR SUPPRESSOR
DE PROTEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
GN CCKN2A OR E1ALPHA OR p16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CANP; TISSUE=SPLEEN;
RX MEDLINE=98151529; PubMed=9482902;
RA Zhang S., Ramsay E.S., Mock B.A.;
RT "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and
RT p19ARF, is a candidate for the plasmacytoma susceptibility locus,
RT pctr1.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
RN [2]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-MA/MAJ;
RX MEDLINE=97179476; PubMed=9021155;
RA Herzog C.R., You M.;
RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
RT suppressor gene.";
RL Mamm. Genome 8:65-66(1997).
RN [3]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-BALB/CJ AND MUS MUS POSCHIAVINUS;
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
RA Pellicer A., Fernandez-Piqueras J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
RT in mouse inbred strains.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF044335; AAC08962.1; -.
DR EMBL: U49279; AAC00051.1; -.
DR EMBL: U79626; AAD00224.1; -.
DR HSSP: P42771; 1B17.
DR MGD: MGI:104738; Cdkn2a.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 4.
DR SMART: SM00248; ANK; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KM ANK repeat; Cyclin; Kinase; Repeat.
SQ SEQUENCE 168 AA: 17915 MW: 356A973BEAC4D167 CRC64.

Query Match 12.8%; Score 19; DB 11; Length 168;
Last Local Similarity 100.0%; Pred. No. 5.1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 RPYHDAAREGFIDTLVYLH 90
DB 72 RPYHDAAREGFIDTLVYLH 90
P97510
P97510 PRELIMINARY; PRT; 168 AA.
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1999 (TREMblrel. 10, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE CYCLIN DEPENDENT KINASE INHIBITOR p16INK4a (p16INK4a TUMOR SUPPRESSOR
DE PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR 2A) (p16INK4a) (CYCLIN-
DE DEPENDENT KINASE INHIBITOR PROTEIN).
GN CCKN2A OR E1ALPHA OR p16INK4A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-DBA/2N; TISSUE=SPLEEN;
RX MEDLINE=98151529; PubMed=9482902;
RA Zhang S., Ramsay E.S., Mock B.A.;
RT "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and
RT p19ARF, is a candidate for the plasmacytoma susceptibility locus,
RT pctr1.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
RN [2]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-DBA/2; AND C57BL/6J X DBA;
RA Malumbres M., de Castro I., Santos J., Melendez B., Manques R.,
RA Serrano M., Pellicer A., Fernandez-Piqueras J.;
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-DBA/2; AND C57BL/6;
RX MEDLINE=95380169; PubMed=7651726;
RA Quelle D.E., Ashmun R.A., Hannon G.J., Reinberger P.A., Trono D.,
RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
RT "Cloning and characterization of murine p16INK4a and p15INK4b genes.";
RL Oncogene 11:635-645(1995).
RN [5]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-DBA/2; AND C57BL/6;
RA Gressani K.M., Rollins L.A., Miller M.S.;
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 1-11 FROM N.A.
RC STRAIN-ICR SWISS;
RX MEDLINE=97128829; PubMed=8973369;
RA Soloff E.V., Herzog C.R., You M.;
RT "The 5'-flanking region of the E1 alpha form of the murine p16INK4a
RT (msl) gene.";
RL Gene 180:213-215(1996).
RN [7]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-CAST/EI, C57BL/6J, ARF/J, AND MOLF/EI;
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
RA Pellicer A., Fernandez-Piqueras J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
RT in mouse inbred strains.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN-129/SVJ;
RA Gong Z., Li J., Fu J.;
RT "Cloning and structure analysis of murine p16INK4a.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF044336; AAC08963.1; -.
DR EMBL: U49280; AAC00052.1; -.
DR EMBL: U66087; AAB39600.1; -.
DR EMBL: U66086; AAB39600.1; JOINED.
DR EMBL: AF004588; AAB61416.1; -.
DR EMBL: U47018; AAC52987.1; -.
DR EMBL: U79628; AAD00226.1; -.
DR EMBL: U79625; AAD00223.1; -.
DR EMBL: U79627; AAD00225.1; -.
DR EMBL: AF332190; AAK83159.1; -.
DR HSSP: P42771; 1B17.
DR MGD: MGI:104738; Cdkn2a.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 4.
DR SMART: SM00248; ANK; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KM ANK repeat; Cyclin; Kinase; Repeat.
SQ SEQUENCE 168 AA: 17915 MW: 356A973BEAC4D167 CRC64.

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SQ SEQUENCE 168 AA; 17941 MW; 9A6B0F24F34D5FEC CRC64;

Query Match 12.8%; Score 19; DB 11; Length 168;

Best Local Similarity 100.0%; Pred. No. 5.1e-10; Mismatches 0; Indels 0; Gaps 0;

QY 72 RPVHDAAREGFLDTLVVL 90  
 |||  
 DB 72 RPVHDAAREGFLDTLVVL 90

RESULT 18

Q9QWH8 PRELIMINARY; PRT; 113 AA.

AC 09QWH8: 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
 GN p16(INK4A).  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;

RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J, RF/J, AND CAST/EI;

RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,

RA Pellicer A., Fernandez-Piqueras J.,

RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences

in mouse inbred strains."

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: U79630; AAD00227.1; -

DR HSSP: P42771; 1B17.

DR InterPro: IPR002110; ANK.

DR Pfam: PF00023; ank; 2.

DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.

KW ANK repeat; Kinase; Repeat.

FT NON\_TER 1 113

FT SEQUENCE 113 AA; 12048 MW; C3A8CF025B94F79E CRC64;

Query Match 12.2%; Score 18; DB 11; Length 113;

Best Local Similarity 100.0%; Pred. No. 3.2e-09; Mismatches 0; Indels 0; Gaps 0;

QY 72 RPVHDAAREGFLDTLVVL 89  
 |||  
 DB 30 RPVHDAAREGFLDTLVVL 47

RESULT 19

Q9QWH7 PRELIMINARY; PRT; 113 AA.

AC 09QWH7: 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).

GN p16(INK4A).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=BALB/CJ;

RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,

RA Pellicer A., Fernandez-Piqueras J.,

RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences

in mouse inbred strains."

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: U79631; AAD00228.1; -

DR HSSP: P42771; 1B17.

DR InterPro: IPR002110; ANK.

DR Pfam: PF00023; ank; 2.

DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.

KW ANK repeat; Kinase; Repeat.

FT NON\_TER 1 113

FT SEQUENCE 113 AA; 12062 MW; DA99452AF91EC60D CRC64;

Query Match 12.2%; Score 18; DB 11; Length 113;

Best Local Similarity 100.0%; Pred. No. 3.2e-09; Mismatches 0; Indels 0; Gaps 0;

QY 72 RPVHDAAREGFLDTLVVL 89  
 |||  
 DB 30 RPVHDAAREGFLDTLVVL 47

RESULT 20

Q9QWH6 PRELIMINARY; PRT; 113 AA.

AC 09QWH6: 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).

GN p16(INK4A).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=MOLF/EI;

RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,

RA Pellicer A., Fernandez-Piqueras J.,

RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences

in mouse inbred strains."

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: U79632; AAD00229.1; -

DR HSSP: P42771; 1B17.

DR InterPro: IPR002110; ANK.

DR Pfam: PF00023; ank; 2.

DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.

KW ANK repeat; Kinase; Repeat.

FT NON\_TER 1 113

FT SEQUENCE 113 AA; 12147 MW; C3A8CF025FD4B39E CRC64;

Query Match 12.2%; Score 18; DB 11; Length 113;

Best Local Similarity 100.0%; Pred. No. 3.2e-09; Mismatches 0; Indels 0; Gaps 0;

QY 72 RPVHDAAREGFLDTLVVL 89  
 |||  
 DB 30 RPVHDAAREGFLDTLVVL 47

RESULT 21

Q97886 PRELIMINARY; PRT; 58 AA.

AC 097886: 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE CYCLIN-DEPENDENT KINASE 2A INHIBITOR (FRAGMENT).

GN CDKN2A.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SKIN;  
 RA Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;  
 RT "An equine sequence homologous to cyclin-dependent kinase inhibitor  
 (CDKN2A).";  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF076782; AAC97110.1;  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 1.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 RW ANK repeat; Kinase; Repeat.  
 FT NON\_TER 1 58  
 FT SEQUENCE 58 AA; 6162 MW; DP9D90C873C1E6D7 CRC64;

Query Match 10.1%; Score 15; DB 6; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 LTRPVHDAREGFL 83  
 Db 44 LTRPVHDAREGFL 58

RESULT 22  
 Q90WH5 PRELIMINARY; PRT; 113 AA.

AC Q90WH5;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
 GN p16(INK4a).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MUS MUS MUSCULUS;  
 RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
 RA Pellicer A., Fernandez-Piqueras J.;  
 RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
 in mouse inbred strains";  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U79633; AAD00230.1;  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 2.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 RW ANK repeat; Kinase; Repeat.  
 FT NON\_TER 1 113  
 FT SEQUENCE 113 AA; 12170 MW; 5D4DE8325D06638B CRC64;

Query Match 10.1%; Score 15; DB 11; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 RPYHDAREGFLDTL 86  
 Db 30 RPYHDAREGFLDTL 44

RESULT 23  
 Q9UD00 PRELIMINARY; PRT; 21 AA.

AC Q9UD00;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE CDKN2 PROTEIN (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95400305; PubMed=7670475;  
 RA Gruis N.A., van der Velde P.A., Sandkuil L.A., Prins D.E.,  
 RA Weaver-Feldhaus J., Kamb A., Bergman W., Frans R.R.;  
 RT "Homologues for CDKN2 (p16) germline mutation in Dutch familial  
 melanoma kindreds";  
 RL Nat. Genet. 10:351-353(1995).  
 SO SEQUENCE 21 AA; 2192 MW; 9424A5E1D7DEAFPS CRC64;

Query Match 9.5%; Score 14; DB 4; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 LLLHGAEPNCADP 67  
 Db 1 LLLHGAEPNCADP 14

RESULT 24  
 Q99PH0 PRELIMINARY; PRT; 144 AA.

AC Q99PH0;  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT CELL CYCLE INHIBITOR (FRAGMENT).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OX Mesocricetus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Muscarella P., Knobloch T.J., Weghorst C.M.;  
 RT "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and  
 RT Identification of Inactivating Alterations in Hamster Tumor Cell  
 Lines";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF291998; AAC59801.1;  
 DR EMBL: AF291997; AAC59801.1; JOINED.  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR SMART: SM00248; ANK; 4.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 RW ANK repeat; Repeat.  
 FT NON\_TER 144 144  
 FT SEQUENCE 144 AA; 15206 MW; 8904F9C0C316A084 CRC64;

Query Match 8.1%; Score 12; DB 11; Length 144;  
 Best Local Similarity 100.0%; Pred. No. 0.0019;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 RPYHDAREGFL 83  
 Db 72 RPYHDAREGFL 83

RESULT 25  
 Q9E033 PRELIMINARY; PRT; 157 AA.

DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR 2.  
OC Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
OC NCBI\_TaxID=10036;  
OX [1]  
RP SEQUENCE FROM N.A.  
RA Muscarella P., Knobloch T.J., Weghorst C.M.:  
RT "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and  
RT Identification of Inactivating Alterations in Hamster Tumor Cell  
RT Lines."  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF292567; AAG44950.1; -.  
DR HSSP; PA2771; 1817.  
DR InterPro; IPR002110; ANK.  
DR SMART; SM00248; ANK; 4.  
DE PROSITE; PS50297; ANK\_REPEAT; 1.  
KW ANK repeat; Kinase; Repeat.  
SQ SEQUENCE 157 AA; 16635 MW; 06FD6A6B30DCF8 CRC64;

Query Match 8.1%; Score 12; DB 11; Length 157;  
Best Local Similarity 100.0%; Pred. No. 0.002;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 RPYHDAREGFL 83  
DB 72 RPYHDAREGFL 83

RESULT 26

ID 09OUJ3 PRELIMINARY; PRT; 44 AA.  
AC 09OUJ3;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).  
GN INK4B.  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RS SEQUENCE FROM N.A.

RA STRAIN-VARIOUS STRAINS;  
RA Santos J., Melendez B., Perez de Castro I., Martin-Rivera L.,  
RA Malumbres M., Serrano M., Pellicer A., Fernandez-Piqueras J.;  
RT "Comparative analysis of the p16 (INK4a) and p15 (INK4b) DNA sequences  
RT in mouse inbred strains."  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U80415; AAD00358.1; -.  
DR EMBL; U80413; AAD00356.1; -.  
DR EMBL; U80414; AAD00357.1; -.  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 1.  
DR SMART; SM00248; ANK; 1.  
DR PROSITE; PS50088; ANK\_REPEAT; 1.  
DR PROSITE; PS50297; ANK\_REPEAT; 1.  
DR ANK repeat; Cyclin; Kinase; Repeat.  
KW NON\_TER 44  
FT NON\_TER 44  
SQ SEQUENCE 44 AA; 4537 MW; AFBFB6B347AB8B34 CRC64;

Query Match 5.4%; Score 8; DB 11; Length 44;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LATTAARG 15

DB 10 LATTAARG 17

RESULT 27

ID 09ZIC0 PRELIMINARY; PRT; 44 AA.  
AC 09ZIC0;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).  
GN INK4B.

OS Mus spretus (Western wild mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10096;  
RN [1]  
RP SEQUENCE FROM N.A.

RA STRAIN-SPRET/EL;  
RA Santos J., Melendez B., Perez de Castro I., Martin-Rivera L.,  
RA Malumbres M., Serrano M., Pellicer A., Fernandez-Piqueras J.;  
RT "Comparative analysis of the p16 (INK4a) and p15 (INK4b) DNA sequences  
RT in mouse inbred strains."  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
RL EMBL; U80416; AAD00359.1; -.  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 1.  
DR SMART; SM00248; ANK; 1.

DR PROSITE; PS50088; ANK\_REPEAT; 1.  
DR PROSITE; PS50297; ANK\_REPEAT; 1.  
KW ANK repeat; Kinase; Repeat.  
FT NON\_TER 44  
SQ SEQUENCE 44 AA; 4537 MW; AFBFB6B347AB8B34 CRC64;

Query Match 5.4%; Score 8; DB 11; Length 44;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LATTAARG 15  
DB 10 LATTAARG 17

RESULT 28

ID 09WLJ9 PRELIMINARY; PRT; 91 AA.  
AC 09WLJ9;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE NONSTRUCTURAL POLYPROTEIN (FRAGMENT).  
OS Hepatitis E virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage.  
OX NCBI\_TaxID=12461;  
RN [1]  
RS SEQUENCE FROM N.A.

RA STRAIN=BCN;  
RA MEDLINE=99013657; PubMed=9797311.  
RA Pina S., Jofre J., Emerson S.U., Purcell R.H., Girones R.;  
RT "Characterization of a strain of infectious hepatitis E virus isolated  
RT from sewage in an area where hepatitis E is not endemic."  
RL Appl. Environ. Microbiol. 64:4485-4488(1998).  
DR EMBL; AF061581; AAC77806.1; -.

KW Polyprotein.  
FT NON\_TER 1  
FT NON\_TER 91  
SQ SEQUENCE 91 AA; 10056 MW; 9017B9EC0CBA3A43 CRC64;

Query Match 5.4%; Score 8; DB 12; Length 91;  
Best Local Similarity 100.0%; Pred. No. 7.5;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 LAELGHR 116  
|||||||

Db 7 LAELGHR 14

RESULT 29

ID 09M618 PRELIMINARY; PRT; 124 AA.

AC 09M618:

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE P13CDKN2X.

GN CDKN2X.

OS Xiphophorus helleri.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Cyprinodontiformes; Poeciliidae; Xiphophorus.

NCBI\_Taxid=8084;

SEQUENCE FROM N.A.  
[1]

RP STRAIN-RIO SARABIA.

RA Kazianis S., Morizot D.C., Della Coletta L., Johnston D.A., Woolcock B., Vielkind J.R., Nairn R.S.;

RT "Comparative Structure and Characterization of a CDKN2 Gene in a Xiphophorus Fish Melanoma Model."

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF132500; MAD21313.1; -.

DR HSSP; P42771; 1B17.

DR InterPro; IPR002110; ANK.

DR Pfam; PF00023; ank; 3.

DR SMART; SM00248; ANK; 1.

DR PROSITE; PS50088; ANK\_REPEAT; 1.

DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.

KW ANK repeat; Repeat.

SQ SEQUENCE 124 AA; 13049 MW; 47F354B1BD27BD3F CRC64;

Query Match 5.4%; Score 8; DB 13; Length 124;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IOVMMGMS 48  
|||||||

Db 40 IOVMMGMS 47

RESULT 30

ID P70067 PRELIMINARY; PRT; 124 AA.

AC P70067:

DT 01-FEB-1997 (TREMBLrel. 02, Created)

DT 01-MAY-1997 (TREMBLrel. 10, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE I3CDKN2X PROTEIN.

GN CDKN2X.

OS Xiphophorus maculatus (Southern platyfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Cyprinodontiformes; Poeciliidae; Xiphophorus.

NCBI\_Taxid=8083;

SEQUENCE FROM N.A.  
[1]

RP STRAIN-UP 163 A; TISSUE=MUSCLE;

RA MEDLINE=9707515; PubMed=8917541;

RA Nairn R.S., Kazianis S., McEntire B.B., Della Coletta L., Walter R.B., Morizot D.C.;

RT "A CDKN2-like polymorphism in Xiphophorus LG V is associated with UV-B-induced melanoma formation in platyfish-swordtail hybrids."

RP STRAIN-HG52;

RL Proc. Natl. Acad. Sci. U.S.A. 93:13042-13047(1996).  
[2]

RP SEQUENCE FROM N.A.

RC STRAIN-UP 163 A; TISSUE=MUSCLE;

RA Kazianis S., Morizot D.C., Della Coletta L., Johnston D.A., Woolcock B., Vielkind J.R., Nairn R.S.;

RT "Comparative Structure and Characterization of a CDKN2 Gene in a Xiphophorus Fish Melanoma Model."

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; U69273; AAB09560.3; -.

DR HSSP; P42771; 1B17.

DR InterPro; IPR002110; ANK.

DR Pfam; PF00023; ank; 3.

DR SMART; SM00248; ANK; 1.

DR PROSITE; PS50088; ANK\_REPEAT; 2.

DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.

KW ANK repeat; Repeat.

SQ SEQUENCE 124 AA; 13034 MW; 47FCBC093707BD25 CRC64;

Query Match 5.4%; Score 8; DB 13; Length 124;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IOVMMGMS 48  
|||||||

Db 40 IOVMMGMS 47

RESULT 31

ID P89468 PRELIMINARY; PRT; 300 AA.

AC P89468:

DT 01-MAY-1997 (TREMBLrel. 03, Created)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE TEGUMENT PROTEIN.

GN UL49.

OS Herpes simplex virus (type 2).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.

OX NCBI\_Taxid=10310;

SEQUENCE FROM N.A.  
[1]

RC STRAIN-HG52;

RA MEDLINE=87111457; PubMed=3027242;

RA McGeoch D.J., Moss H.W., McNab D., Frame M.C.;

RT "DNA sequence and genetic content of the HindIII 1 region in the short unique component of the herpes simplex virus type 2 genome: identification of the gene encoding glycoprotein G, and evolutionary comparisons."

RT J. Gen. Virol. 68:19-38(1987).  
[2]

RP SEQUENCE FROM N.A.

RC STRAIN-HG52;

RA MEDLINE=90278430; PubMed=2161906;

RA Everett R., Fenwick M.;

RT "Comparative DNA sequence analysis of the host shutoff genes of different strains of herpes simplex virus: type 2 strain HG52 encodes a truncated UL41 product."

RL J. Gen. Virol. 71:1387-1390(1990).  
[3]

RP SEQUENCE FROM N.A.

RC STRAIN-HG52;

RA MEDLINE=92113549; PubMed=1662697;

RA McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;

RT "Comparative sequence analysis of the long repeat regions and adjoining parts of the long unique regions in the genomes of herpes simplex viruses types 1 and 2."

RT J. Gen. Virol. 72:3057-3075(1991).  
[4]

RP SEQUENCE FROM N.A.

RC STRAIN-HG52;